

SEQUENCE LISTING

(1) GENERAL INFORMATION:



(i) APPLICANT: Jacobs, Kenneth
 McCoy, John M.
 LaVallie, Edward R.
 Racie, Lisa A.
 Treacy, Maurice
 Spaulding, Vikki
 Agostino, Michael J.
 Howes, Steven H.
 Fechtel, Kim

(ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
 ENCODING THEM

(iii) NUMBER OF SEQUENCES: 231

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
 (B) STREET: 87 CambridgePark Drive
 (C) CITY: Cambridge
 (D) STATE: MA
 (E) COUNTRY: U.S.A.
 (F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/746,783
 (B) FILING DATE: 2000-DEC-21
 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Milasincic, Debra J.
 (B) REGISTRATION NUMBER: 46,931

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2043 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGAATGCCC CATGCGCACC CCACAGCTCG CGCTCCTGCA AGTGTTCTTT CTGGTGTTC

CCGATGGCGT CCGGCCTCAG CCCTCTTCCT CCCCATCAGG GGCAGTGCCC ACGTCTTTGG	120
AGCTGCAGCG AGGGACGGAT GGCGBAACCC TCCAGTCCCC TTCAGAGGCG ACTGCAACTC	180
GGCCGGCCGT GCCTGGACTC CCTACAGTGG TCCCTACTCT CGTGA CTCCC TCGGCCCTG	240
GGAATAGGAC TGTGGACCTC TTCCCAGTCT TACCGATCTG TGTCTGTGAC TTGACTCCTG	300
GAGCCTGCGA TATAAATTGC TGCTGCGACA GGGACTGCTA TCTTCTCCAT CCGAGGACAG	360
TTTTCTCCTT CTGCCTTCCA GGCAGCGTAA GGTCTTCAAG CTGGGTTTGT GTAGACAACT	420
CTGTTATCTT CAGGAGTAAT TCCCCGTTTC CTTCAAGAGT TTTCATGGAT TCTAATGGAA	480
TCAGGCAGTT TTGTGTCCAT GTGAACAACT CAAACTTAAA CTATTTCCAG AAGCTTCAAA	540
AGGTCAATGC AACCAACTTC CAGGCCCTGG TTGCAGAGTT TGGAGGCGAA TCATTCACTT	600
CAACATTCCA AACTCAATCA CCACCATCTT TTTACAGGGC CGGGGACCCC ATTCTTACTT	660
ACTTCCCCAA GTGGTCTGTA ATAAGCTTGC TGAGACAACC TGCAGGAGTT GGAGCTGGGG	720
GACTCTGTGC TGAAAGCAAT CCTGCAGGTT TCCTAGAGAG TAAAAGTACA ACTTGCACTC	780
GTTTTTTTCA AGAACCTGGC TAGTAGCTGT ACCTTGGATT CAGCCCTCAA TGCTGCCTCT	840
TACTATAACT TCACAGTCTT AAAGGTTCCA AGAAGCATGA CTGATCCACA GAATATGGAG	900
TTCCAGGTTT CTGTAATACT TACCTCACAG GCTAATGCTC CTCTGTTGGC TGGAAACACT	960
TGTCAGAATG TAGTTTCTCA GGTACCTAT GAGATAGAGA CCAATGGGAC TTTTGAATC	1020
CAGAAAGTTT CTGTCAGTTT GGGACAAACC AACCTGACTG TTGAGCCAGG CGCTTCCTTA	1080
CAGCAACACT TCATCCTTCG CTTCAGGGCT TTTCAACAGA GCACAGCTGC TTCTCTCACC	1140
AGTCCTAGAA GTGGGAATCC TGGCTATATA GTTGGGAAGC CACTCTTGGC TCTGACTGAT	1200
GATATAAGTT ACTCAATGAC CCTCTTACAG AGCCAGGGTA ATGGAAGTTG CTCTGTTAAA	1260
AGACATGAAG TGCAGTTTGG AGTGAATGCA ATATCTGGAT GCAAGCTCAG GTTGAAGAAG	1320
GCAGACTGCA GCCACTTGCA GCAGGAGATT TATCAGACTC TTCATGGAAG GCCCAGACCA	1380
GAGTATGTTG CCATCTTTGG TAATGCTGAC CCAGCCCAGA AAGGAGGGTG GACCAGGATC	1440
CTCAACAGGC ACTGCAGCAT TTCAGCTATA AACTGTACTT CCTGCTGTCT CATACCAGTT	1500
TCCCTGGAGA TCCAGGTATT GTGGGCATAT GTAGGTCTCC TGTCCAACCC GCAAGCTCAT	1560
GTATCAGGAG TTCGATTCTT ATACCAGTGC CAGTCTATAC AGGATTCTCA GCAAGTTACA	1620
GAAGTATCTT TGACAACTCT TGTGAACTTT GTGGACATTA CCCAGAAGCC ACAGCCTCCA	1680
AGGGGCCAAC CCAAATGGA CTGGAAATGG CCATTCGACT TCTTTCCCTT CAAAGTGGCA	1740
TTCAGCAGAG GAGTATTCTC TCAAAAATGC TCAGTCTCTC CCATCCTTAT CCTGTGCCTC	1800
TTAGAACTTG GAGTTCTCAA CCTAGAGACT ATGTGAAGAA AAGAAAATAA TCAGATTTC	1860
GTTTTCCCTA TGAGAACTC TGAGGCAGCC ACTTATCTTG GCTAAATAGA ACCTCACCTG	1920

CTCATGACCA GAGAGCATTT AGGATAATAG AGGACCTAAC TGAAGGAATC CTTGTATATG 1980
 AAAGGAGTTA TTTTAGAAAA GCAATAAAAA TATTTTATTC ATCATAAAAA AAAAAAAAAA 2040
 AAA 2043

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Thr Pro Gln Leu Ala Leu Leu Gln Val Phe Phe Leu Val Phe
 1 5 10 15
 Pro Asp Gly Val Arg Pro Gln Pro Ser Ser Ser Pro Ser Gly Ala Val
 20 25 30
 Pro Thr Ser Leu Glu Leu Gln Arg Gly Thr Asp Gly Gly Thr Leu Gln
 35 40 45
 Ser Pro Ser Glu Ala Thr Ala Thr Arg Pro Ala Val Pro Gly Leu Pro
 50 55 60
 Thr Val Val Pro Thr Leu Val Thr Pro Ser Ala Pro Gly Asn Arg Thr
 65 70 75 80
 Val Asp Leu Phe Pro Val Leu Pro Ile Cys Val Cys Asp Leu Thr Pro
 85 90 95
 Gly Ala Cys Asp Ile Asn Cys Cys Cys Asp Arg Asp Cys Tyr Leu Leu
 100 105 110
 His Pro Arg Thr Val Phe Ser Phe Cys Leu Pro Gly Ser Val Arg Ser
 115 120 125
 Ser Ser Trp Val Cys Val Asp Asn Ser Val Ile Phe Arg Ser Asn Ser
 130 135 140
 Pro Phe Pro Ser Arg Val Phe Met Asp Ser Asn Gly Ile Arg Gln Phe
 145 150 155 160
 Cys Val His Val Asn Asn Ser Asn Leu Asn Tyr Phe Gln Lys Leu Gln
 165 170 175
 Lys Val Asn Ala Thr Asn Phe Gln Ala Leu Val Ala Glu Phe Gly Gly
 180 185 190
 Glu Ser Phe Thr Ser Thr Phe Gln Thr Gln Ser Pro Pro Ser Phe Tyr
 195 200 205
 Arg Ala Gly Asp Pro Ile Leu Thr Tyr Phe Pro Lys Trp Ser Val Ile
 210 215 220

ATTY DOCKET NO.: GIN-6054CP

Ser Leu Leu Arg Gln Pro Ala Gly Val Gly Ala Gly Gly Leu Cys Ala
 225 230 235 240

Glu Ser Asn Pro Ala Gly Phe Leu Glu Ser Lys Ser Thr Thr Cys Thr
 245 250 255

Arg Phe Phe Gln Glu Pro Gly
 260

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGCAGCTCA TCAACCCCTT TGGAGAGGAT GATGATGATT TTGAGACCAA CTGGATTGTC	60
GACAGGAATT TGCAGGTGTC CCTGTTGGCT GTGGATGAGA TGCACCAGGA CCTGCCTCGG	120
ATGGAGCCGG ACATGTACTG GAATAAGCCC GAGCCACAGC CCCCCTACAC AGCTGCTTCC	180
CCCCAGTTCC GTCGAGCCTC CTTTATGGGC TCCACCTTCA ACATCAGCCT GAACAAAGAG	240
GAGATGGAGT TCCAGCCCAA TCAGGAGGAC GAGGAGGATG CTCACGCTGG CATCATTGGC	300
CGCTTCCTAG GCCTGCAGTC CCATGATCAC CATCCTCCCA GGGCAAATC AAGGACCAAA	360
CTACTGTGGC CCAAGAGGGA ATCCCTTCTC CACGAGGGCC TGCCCAAAAA CCACAAGGCA	420
GCCAAACAGA ACGTTAGGGG CCAGGAAGAC AACAAGGCCT GGAAGCTTAA GGCTGTGGAC	480
GCCTTCAAGT CTGCCCCACT GTATCAGAGG CCAGGCTACT ACAGTGCCCC ACAGACGCCC	540
CTCAGCCCCA CTCCCATGTT CTTCCCCCTA GAACCATCAG CGCCGTCAAA GCTTCACAGT	600
GTACAGGCA TAGACACCAA AGACAAAAGC TTAAAGACTG TGAGTTCTGG GGCCAAGAAA	660
AGTTTTGAAT TGCTCTCAGA GAGCGATGGG GCCTTGATGG AGCACCAGAG AGTATCTCAA	720
GTGAGGAGGA AACTGTGGA GTTTAACCTG ACGGATATGC CAGAGATCCC CGAAAATCAC	780
CTCAAAGAAC CTTTGGAACA ATCACCAACC AACATACACA CTACACTCAA AGATCACATG	840
GATCCTTATT GGGCCTTGGA AAACAGGGAT GAAGCACATT CCTAACCTGC TTCCTAATGG	900
GGATGCTTCG CCAGCCAGGT CCTCACCTGT GTGTACACCA GCAGGACACT GATCCAGTCA	960
CAGCCATACA GCTGTCCACA CTGAAGAACA TGTCTACAA CAGCCTGAAT CAAATGGCTA	1020
GCTTAATAGA TAAAAATCCC AGACTACTTC AGCCTTTAAT GCCTTTTATT CATAAAAACT	1080
GTGAAAGCTA GACTGAACCA TTGGAAACAT TTAATCAGA CTCTGGATTC AGAGTCGGGA	1140
ACCCTTAGTT CTATCTGAAT CCAAGACAGC CACACCTTAG TATACTGCCC AACTAATGA	1200

ATTY DOCKET NO.: GIN-6054CP

GTTTAATAAA TACAAATACT CGTTAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1260
 AAA 1263

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	His	Gln	Asp	Leu	Pro	Arg	Met	Glu	Pro	Asp	Met	Tyr	Trp	Asn	Lys	1	5	10	15
Pro	Glu	Pro	Gln	Pro	Pro	Tyr	Thr	Ala	Ala	Ser	Ala	Gln	Phe	Arg	Arg	20	25	30	
Ala	Ser	Phe	Met	Gly	Ser	Thr	Phe	Asn	Ile	Ser	Leu	Asn	Lys	Glu	Glu	35	40	45	
Met	Glu	Phe	Gln	Pro	Asn	Gln	Glu	Asp	Glu	Glu	Asp	Ala	His	Ala	Gly	50	55	60	
Ile	Ile	Gly	Arg	Phe	Leu	Gly	Leu	Gln	Ser	His	Asp	His	His	Pro	Pro	65	70	75	80
Arg	Ala	Asn	Ser	Arg	Thr	Lys	Leu	Leu	Trp	Pro	Lys	Arg	Glu	Ser	Leu	85	90	95	
Leu	His	Glu	Gly	Leu	Pro	Lys	Asn	His	Lys	Ala	Ala	Lys	Gln	Asn	Val	100	105	110	
Arg	Gly	Gln	Glu	Asp	Asn	Lys	Ala	Trp	Lys	Leu	Lys	Ala	Val	Asp	Ala	115	120	125	
Phe	Lys	Ser	Ala	Pro	Leu	Tyr	Gln	Arg	Pro	Gly	Tyr	Tyr	Ser	Ala	Pro	130	135	140	
Gln	Thr	Pro	Leu	Ser	Pro	Thr	Pro	Met	Phe	Phe	Pro	Leu	Glu	Pro	Ser	145	150	155	160
Ala	Pro	Ser	Lys	Leu	His	Ser	Val	Thr	Gly	Ile	Asp	Thr	Lys	Asp	Lys	165	170	175	
Ser	Leu	Lys	Thr	Val	Ser	Ser	Gly	Ala	Lys	Lys	Ser	Phe	Glu	Leu	Leu	180	185	190	
Ser	Glu	Ser	Asp	Gly	Ala	Leu	Met	Glu	His	Pro	Glu	Val	Ser	Gln	Val	195	200	205	
Arg	Arg	Lys	Thr	Val	Glu	Phe	Asn	Leu	Thr	Asp	Met	Pro	Glu	Ile	Pro	210	215	220	
Glu	Asn	His	Leu	Lys	Glu	Pro	Leu	Glu	Gln	Ser	Pro	Thr	Asn	Ile	His	225	230	235	240

ATTY DOCKET NO.: GIN-6054CP

Thr Thr Leu Lys Asp His Met Asp Pro Tyr Trp Ala Leu Glu Asn Arg
245 250 255

Asp Glu Ala His Ser
260

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTTGAGGGT TTTTGTGTTT TTGTTTTTTC TAGGATTTCA TTGTGATGTT TTGGTTTTGT	60
TTTTTGCTTT TTGTTTAAGT TGTGCTGACA CCAAACACAT CCAGTTTATA ATCAGTACAT	120
TGGAAAGCTG GTATTGATGT AGAACCAGTG CATAACTTTT TATGGGGTTT TGTTATTGGT	180
TTTTTTTTTG TAAAGTGTGA ATAAAAGGTA TGTTTACTCA TTTTTCCTGA ACACTGTGTT	240
GGTAATGTGC ATCATGACAA TTTCCAGTGA AGGTGAGCTG GAGCTGGTTG GACTAATGAG	300
ACTGAGGAAG CAGCTTTTCC TACGATCTGC ATTATGTAAT CACAGGTCCA GAGAGCTTTA	360
TGGAAGCGGG AGAGGAGGAG CACTTACTCA TGTTGTATTT GTTAATGGAG GATGTCATCT	420
TTTCATAGAT GCTGGAAC TA GAGTGCACTT GTTAGATGCT AAAGGTTTGA GCTTTACACA	480
AAATGTCTTC ATCTGTATTT GTTATTGTCT ACAATATATT TGAATTTGGG GCAGCATATT	540
AAGATGTAAT GCCCTGTTAT GTCTGGAAAA AACTTGTTTT GCTTCTTCCA GGCAAAGGGC	600
ATTTTGTGGA TCAGTTTGAA CAGCTTCTCC ACCTTATTTG GACAGTGATA AATTGAACCA	660
AGAGTGTAGA TTTACAAGTG TAACCTTCAA AAGAGGAAGA ACTATTTGGG GTCTGTAGGT	720
AATGAACAGT CACACCAAAA TAGACTATGA TGCTTTTGTT AAGAAAGGTT TCATGTTTTA	780
GATATTTTCC GTGTCCTAAA TAATTTTCAA TAATCTATAA TCCCTAAAAT GCAATAAAAA	840
CTAGTATGTT TTCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA	894

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Cys Ile Met Thr Ile Ser Ser Glu Gly Glu Leu Glu Leu Val Gly

ATTY DOCKET NO.: GIN-6054CP

1	5	10	15
Leu Met Arg	Leu Arg Lys Gln Leu Phe	Leu Arg Ser Ala	Leu Cys Asn
20	25	30	
His Arg Ser	Arg Glu Leu Tyr Gly	Ser Gly Arg Gly	Gly Ala Leu Thr
35	40	45	
His Val Val	Phe Val Asn Gly Gly	Cys His Leu Phe	Ile Asp Ala Gly
50	55	60	
Thr Arg Val	His Leu Leu Asp Ala Lys	Gly Leu Ser Phe	Thr Gln Asn
65	70	75	80
Val Phe Ile	Cys Ile Cys Tyr Cys	Leu Gln Tyr Ile	
85	90		

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 784 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGCCGCAG GTCTACTTGT GGCGAGCAGT CCAGCACAGC CTCACAGTGC AGAGCATGAG	60
CTTTGGAGCC TGCCCCCACC CTAGCTTTGT GACCTTAAGT GAGCTACATA GCTTCTCATG	120
TGTAAACTAC TCATCATAAT GGTTCTGACC TCAGTGGTTT GTTGTGTTCT AGGAAATGAT	180
GCCAGTGAAT GCGTAGTCCC AGCCTCAGCA CAGGGGAGCC ACCTTGAAGC TCTCAAATAT	240
CACTGTTGTG AATACAGAGA GGGAAAACCA ACTGTAACGT GCCACCCAAA TTTTTCAGA	300
TTAATACATC ATTCATCAGA CTTCATTCGT GATCTCGAAG AGTGACATCA GTCTTCCTTG	360
GAATATGAAG AGAATTTCTT TGGTTCTTCT TTTGCATTTC TATTTGATTT ATTTTATTTT	420
ATTTTATTTT ATGTTTTTTG GTACAGAAAG CTCATTACTA GTCCTGTCCA GCAACGTGCC	480
TCTCCTGGCC CTAGAGTTCT TGGAAATAGC CCAGGCCAAA GAGAAGGCCT TTCTCCCCAT	540
GGTCAGCCAC ACGTTCCACA TGCGCACAGA GGAGTCTGAT GCCTCACAGG AGGGCGATGA	600
CCTACCCAAG TCCTCAGCAA ACACCAGCCA TCCAAGCAG GATGACAGCC CCAAGTCCTC	660
AGAAGAAACC ATCCAGCCCA AGGAGGGTGA CATCCCCAAG GCCCCAGAAG AAACCATCCA	720
ATCCAAGAAG GAGGACCTCC CCAAGTCCTC GGAAAAAGCC ATCCAGCCCA AAGAGAGTAA	780
CATC	784

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids

ATTY DOCKET NO.: GIN-6054CP

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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Met Lys Arg Ile Ser Leu Val Leu Leu Leu His Phe Tyr Leu Ile Tyr
1           5           10           15

Phe Ile Leu Phe Tyr Phe Met Phe Phe Gly Thr Glu Ser Ser Leu Leu
20           25           30

Val Leu Ser Ser Asn Val Pro Leu Leu Ala Leu Glu Phe Leu Glu Ile
35           40           45

Ala Gln Ala Lys Glu Lys Ala Phe Leu Pro Met Val Ser His Thr Phe
50           55           60

His Met Arg Thr Glu Glu Ser Asp Ala Ser Gln Glu Gly Asp Asp Leu
65           70           75           80

Pro Lys Ser Ser Ala Asn Thr Ser His Pro Lys Gln Asp Asp Ser Pro
85           90           95

Lys Ser Ser Glu Glu Thr Ile Gln Pro Lys Glu Gly Asp Ile Pro Lys
100          105          110

Ala Pro Glu Glu Thr Ile Gln Ser Lys Lys Glu Asp Leu Pro Lys Ser
115          120          125

Ser Glu Lys Ala Ile Gln Pro Lys Glu Ser Asn Ile
130          135          140

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      60
AAAAAAAAAA AAAAAA                                         75

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 939 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

ATTY DOCKET NO.: GIN-6054CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGAAGAAGTA GAAGCATCGA AAGCGTTGGA GAGGTGTTAC CGGAACGGCG GCGACAAGGG	60
TGTTCCCGAA CTAGAGTGGG GCATACATAA TCTTGCTGCT ATGCTTCGAA GCTGTAGTCT	120
GAATCAACCT AAGTTTTTAAA CAGAAGGTGA ACCTCTGAGA TAGAAAATCA AGTATATTTT	180
AAAAGAAGGG ATGTGGGATC AAGGAGGACA GCCTTGCCAG CAGTGGCCCT TGAACCAGCA	240
ACAATGGATG CAGTCATTCC AGCACCAACA GGATCCAAGC CAGATTGATT GGGCTGCATT	300
GGCCCAAGCT TGGATTGCCC AAAGAGAAGC TTCAGGACAG CAAAGCATGG TAGAACAACC	360
ACCAGGAATG ATGCCAAATG GACAAGATAT GTCTACAATG GAATCTGGTC CAAACAATCA	420
TGGGAATTTT CAAGGGGATT CAAACTTCAA CAGAATGTGG CAACCAGAAT GGGGAATGCA	480
TCAGCAACCC CCACACCCCC CTCCAGATCA GCCATGGATG CCACCAACAC CAGGCCCAAT	540
GGACATTGTT CCTCCTTCTG AAGACAGCAA CAGTCAGGAC AGTGGGGAAT TTGCCCCCTGA	600
CAACAGGCAT ATATTTAACC AGAACAATCA CAACTTTGGT GGACCACCCG ATAATTTTGC	660
AGTGGGGCCA GTGAACCAGT TTGACTATCA GGACCTCCAG GACCTCCAGC ACCTCCCCAG	720
AATCGAAGAG AAAGGCCATC ATCATTGAGG GATCGTCAGC GTTCACCTAT TGCACTTCCT	780
GTGAAGCAGG AGCCTCCACA AATTGACGCA GTAAACGCA GGACTCTTCC CGCTTGGATT	840
CGCGAAGGTC TTGAAAAAAT GGAACGTGAA AAGCAGAAGA AATTGGAGAA AGAAAGAATG	900
GAACAACAAC GTTCACAATT GTCCAAAAAA AAAAAAAAAA	939

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Trp Asp Gln Gly Gly Gln Pro Trp Gln Gln Trp Pro Leu Asn Gln	
1 5 10 15	
Gln Gln Trp Met Gln Ser Phe Gln His Gln Gln Asp Pro Ser Gln Ile	
20 25 30	
Asp Trp Ala Ala Leu Ala Gln Ala Trp Ile Ala Gln Arg Glu Ala Ser	
35 40 45	
Gly Gln Gln Ser Met Val Glu Gln Pro Pro Gly Met Met Pro Asn Gly	
50 55 60	
Gln Asp Met Ser Thr Met Glu Ser Gly Pro Asn Asn His Gly Asn Phe	
65 70 75 80	

ATTY DOCKET NO.: GIN-6054CP

Gln Gly Asp Ser Asn Phe Asn Arg Met Trp Gln Pro Glu Trp Gly Met
85 90 95

His Gln Gln Pro Pro His Pro Pro Pro Asp Gln Pro Trp Met Pro Pro
100 105 110

Thr Pro Gly Pro Met Asp Ile Val Pro Pro Ser Glu Asp Ser Asn Ser
115 120 125

Gln Asp Ser Gly Glu Phe Ala Pro Asp Asn Arg His Ile Phe Asn Gln
130 135 140

Asn Asn His Asn Phe Gly Gly Pro Pro Asp Asn Phe Ala Val Gly Pro
145 150 155 160

Val Asn Gln Phe Asp Tyr Gln Asp Leu Gln Asp Leu Gln His Leu Pro
165 170 175

Arg Ile Glu Glu Lys Gly His His His Ser Gly Ile Val Ser Val His
180 185 190

Leu Leu His Phe Leu
195

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGGAGAGCAG CCGGCAGCGC CTGGAGGCCC TGAGAGAGCT GCAATAAAGG AAGAAACAGA	60
ATATATGGAA CTTCTGGCAG CAGAAAAACA TCAAGTTGAA GCCCTTAAAA ATATGCAACA	120
TCAAAACCAA AGTTTATCCA TGCTTGACGA GATTCTTGAA GATGTAAGAA AGGCAGCGGA	180
TCGTCTGGAG GAAGAGATAG AGGAACATGC TTTTGACGAC AATAAATCAG TCAAGGGGGT	240
CAATTTTGAG GCAGTTCTGA GGGTGGAGGA AGAAGAGGCC AATTCTAAGC AAAATATAAC	300
AAAACGAGAA GTGGAGGATG ACTTGGGTCT TAGCATGCTG ATTGACTCCC AGAACAACCA	360
GTATATTTTG ACCAAGCCCA GAGATTCAAC CATCCCACGT GCAGATCACC ACTTTATAAA	420
GGACATTGTT ACCATAGGAA TGCTGTCCTT GCCTTGTTGGC TGGCTATGTA CAGCCATAGG	480
ATTGCCTACA ATGTTTGGTT ATATTATTTG TGGTGTACTT CTGGGACCTT CAGGACTAAA	540
TAGTATTAAG TCTATTGTGC AAGTGGAGAC ATTAGGAGAA TTTGGGGTGT TTTTACTCT	600
TTTCTTGTT GGCTTAGAAT TTTCTCCAGA AAAGCTAAGA AAGGTGTGGA AGATTCCTT	660
ACAAGGGCCG TGTTACATGA CACTGTTAAT GATTGCATTT GGCTTGCTGT GGGGGCATCT	720
CTTGCGGATC AAACCCACGC AGAGCGTCTT CATTTCCACG TGTCTGTCCT TGTCAGCAC	780

ACCCCTCGTG TCCAGGTTCC TCATGGGCAG TGCTCGGGGT GACAAAGAAG GCGACATTGA	840
CTACAGCACC GTGCTCCTCG GCATGCTGGT GACGCAGGAC GTGCAGCTCG GGCTCTTCAT	900
GGCCGTCATG CCGACTCTCA TACAGGCGGG CGCCAGTGCA TCTTCTAGCA TTGTCGTGGA	960
AGTTCTCCGA ATCCTGGTTT TGATTGGTCA GATTCTTTTT TCCTAGCGG CGGTTTTTCT	1020
TTTATGTCTT GTTATAAAGA AGTATCTCAT TGGACCCTAT TATCGGAAGC TGCACATGGA	1080
AAGCAAGGGG AACAAAGAAA TCCTGATCTT GGGAATATCT GCCTTTATCT TCTTAATGTT	1140
AACGGTCACG GAGCTGCTGG ACGTCTCCAT GGAGCTGGGC TGTTTCCTGG CTGGAGCGCT	1200
CGTCTCCTCT CAGGGCCCCG TGGTCACCGA GGAGATCGCC ACCTCCATCG AACCCTATCCG	1260
CGACTTCCTG GCCATCGTTT TCTTCGCCTC CATAGGGCTC CACGTGTTCC CCACGTTTGT	1320
GGCGTACGAG CTCACGGTGC TGGTGTTCTT CACCTTGTC A GTGGTGGTGA TGAAGTTTCT	1380
CCTGGCGGCG CTGGTCCTGT CTCTCATTCT GCCGAGGAGC AGCCAGTACA TCAAGTGGAT	1440
CGTCTCTGCG GGGCTTGCCC AGGTCAGCGA GTTTTCCTTT GTCCTGGGGA GCCGGGCGCG	1500
AAGAGCGGGC GTCATCTCTC GGGAGGTGTA CCTCCTTATA CTGAGTGTA CCACGCTCAG	1560
CCTCTTGCTC GCCCCGGTGC TGTGGAGAGC TGCAATCACG AGGTGTGTGC CCAGACCGGA	1620
GAGACGGTCC AGCCTCTGAT GGCTCGGAGA TGATGGACCG TGGAAGGGAA GCGTCTGTGG	1680
GGAGTGAGCG CTTAGATGGC CAGCAGCTGC TCCTTCTGGG AAGCTCGCAC CTTGGCAACA	1740
GAACAGCCCT CTAGCAGAGC GTCAGTGAGC TCGTGTTATC CCGGCTTTTA CAGAATATTC	1800
TTGTCCTATT TTAGAATTTT CCGGAGTAGT TTATTTGCAG TCTGTTGATT ATGTGCAGTA	1860
GACCCGGGAC ACTGCGTTTT ACCGATCACC TTGAATGTGG TGCCTGGATG TGCCTTTTTT	1920
TTTTTCCCT GAAATTATTA TTAATTTTCT ATKGKGAGTT CATCAGTTCA TAGTTTTTTT	1980
AGTAAAGAAG CAAATTAATA AGGCTTTTAA AAATGTACAA CTTCAGAATT ATAATCTGTT	2040
AGTCAAATAT TTGTTATTAA ACATTTCTGT AATATGAAGT TGTAATCCTG GCCGTGAGCT	2100
TGGAAGCTTA CTTTTGATTC TTAAAGCCTA TGTTTTCTAA AATGAGACAA ATACGGATGT	2160
CTATTTGCCT TTTATTGTAA CTTTAAATG AAATAATTTT ATGTCAATTT CTATTAGATA	2220
TATCACTTAA AATATTTGGT TTAAATCAC AAGAATATGT ATTCTTTAAT AAAGATAATT	2280
TATGATCATG GTATAATTAA TTGAAATTTA TTAAATCTG TTTTATTAA AAAAAAAAAA	2340
AAA	2343

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Glu	Leu	Leu	Ala	Ala	Glu	Lys	His	Gln	Val	Glu	Ala	Leu	Lys	Asn	1	5	10	15
Met	Gln	His	Gln	Asn	Gln	Ser	Leu	Ser	Met	Leu	Asp	Glu	Ile	Leu	Glu	20	25	30	
Asp	Val	Arg	Lys	Ala	Ala	Asp	Arg	Leu	Glu	Glu	Glu	Ile	Glu	Glu	His	35	40	45	
Ala	Phe	Asp	Asp	Asn	Lys	Ser	Val	Lys	Gly	Val	Asn	Phe	Glu	Ala	Val	50	55	60	
Leu	Arg	Val	Glu	Glu	Glu	Glu	Ala	Asn	Ser	Lys	Gln	Asn	Ile	Thr	Lys	65	70	75	80
Arg	Glu	Val	Glu	Asp	Asp	Leu	Gly	Leu	Ser	Met	Leu	Ile	Asp	Ser	Gln	85	90	95	
Asn	Asn	Gln	Tyr	Ile	Leu	Thr	Lys	Pro	Arg	Asp	Ser	Thr	Ile	Pro	Arg	100	105	110	
Ala	Asp	His	His	Phe	Ile	Lys	Asp	Ile	Val	Thr	Ile	Gly	Met	Leu	Ser	115	120	125	
Leu	Pro	Cys	Gly	Trp	Leu	Cys	Thr	Ala	Ile	Gly	Leu	Pro	Thr	Met	Phe	130	135	140	
Gly	Tyr	Ile	Ile	Cys	Gly	Val	Leu	Leu	Gly	Pro	Ser	Gly	Leu	Asn	Ser	145	150	155	160
Ile	Lys	Ser	Ile	Val	Gln	Val	Glu	Thr	Leu	Gly	Glu	Phe	Gly	Val	Phe	165	170	175	
Phe	Thr	Leu	Phe	Leu	Val	Gly	Leu	Glu	Phe	Ser	Pro	Glu	Lys	Leu	Arg	180	185	190	
Lys	Val	Trp	Lys	Ile	Ser	Leu	Gln	Gly	Pro	Cys	Tyr	Met	Thr	Leu	Leu	195	200	205	
Met	Ile	Ala	Phe	Gly	Leu	Leu	Trp	Gly	His	Leu	Leu	Arg	Ile	Lys	Pro	210	215	220	
Thr	Gln	Ser	Val	Phe	Ile	Ser	Thr	Cys	Leu	Ser	Leu	Ser	Ser	Thr	Pro	225	230	235	240
Leu	Val	Ser	Arg	Phe	Leu	Met	Gly	Ser	Ala	Arg	Gly	Asp	Lys	Glu	Gly	245	250	255	
Asp	Ile	Asp	Tyr	Ser	Thr	Val	Leu	Leu	Gly	Met	Leu	Val	Thr	Gln	Asp	260	265	270	
Val	Gln	Leu	Gly	Leu	Phe	Met	Ala	Val	Met	Pro	Thr	Leu	Ile	Gln	Ala	275	280	285	
Gly	Ala	Ser	Ala	Ser	Ser	Ser	Ile	Val	Val	Glu	Val	Leu	Arg	Ile	Leu				

290	295	300
Val Leu Ile Gly Gln Ile Leu Phe Ser Leu Ala Ala Val Phe Leu Leu		
305	310	315 320
Cys Leu Val Ile Lys Lys Tyr Leu Ile Gly Pro Tyr Tyr Arg Lys Leu		
	325	330 335
His Met Glu Ser Lys Gly Asn Lys Glu Ile Leu Ile Leu Gly Ile Ser		
	340	345 350
Ala Phe Ile Phe Leu Met Leu Thr Val Thr Glu Leu Leu Asp Val Ser		
	355	360 365
Met Glu Leu Gly Cys Phe Leu Ala Gly Ala Leu Val Ser Ser Gln Gly		
	370	375 380
Pro Val Val Thr Glu Glu Ile Ala Thr Ser Ile Glu Pro Ile Arg Asp		
	385	390 395 400
Phe Leu Ala Ile Val Phe Phe Ala Ser Ile Gly Leu His Val Phe Pro		
	405	410 415
Thr Phe Val Ala Tyr Glu Leu Thr Val Leu Val Phe Leu Thr Leu Ser		
	420	425 430
Val Val Val Met Lys Phe Leu Leu Ala Ala Leu Val Leu Ser Leu Ile		
	435	440 445
Leu Pro Arg Ser Ser Gln Tyr Ile Lys Trp Ile Val Ser Ala Gly Leu		
	450	455 460
Ala Gln Val Ser Glu Phe Ser Phe Val Leu Gly Ser Arg Ala Arg Arg		
	465	470 475 480
Ala Gly Val Ile Ser Arg Glu Val Tyr Leu Leu Ile Leu Ser Val Thr		
	485	490 495
Thr Leu Ser Leu Leu Leu Ala Pro Val Leu Trp Arg Ala Ala Ile Thr		
	500	505 510
Arg Cys Val Pro Arg Pro Glu Arg Arg Ser Ser Leu		
	515	520

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCAGCCCGG GCCATGCCGC ACGGCTGCTG ACCGCACGCA GGGGCCGGCC CCGAGGACAC	60
ATGCGGCGGC CTTTGCCGCC TCGCCCCTGA CCCTCTGCCC TGTTCTCCAT GTTGCAATTC	120
TCGTCAGTTT CTCGGGCGGT GTAGCTGCCG CTGCCACCAG AGCCGGCGGG GCATCGCGCT	180

ATTY DOCKET NO.: GIN-6054CP

GCTCATT CAT CCGGCCG CAC TTTCTTTTCC GTTTCACCC ATCCCTTCCC ATTTCTTCT 240
 CCCTTTCCCC GCCAGCTTCG CATCCATCTC CCCCACCCCG TAACCCCTCC TGCCTCCATC 300
 CACCGGGGCT ATTGCCGCAA AAGA 324

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 550 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCTGAACATT TCAGAAATAC AGAAGTTGAA GCAGCAGCTT ATGCAGGTAG AGCGGGAAAA 60
 GGCCATTCTT TTGGCCAACC TACAGGAGTC ACAGACACAG CTGGAACACA CCAAGGGGGC 120
 ACTGACGGAG CAGCATGAGC GGGTGCACCG GCTCACAGAG CACGTCAATG CCATGAGGGG 180
 CCTGCAAAGC AGCAAGGAGC TCAAGGCTGA GCTGGACGGG GAGAAGGGCC GGGACTCAGG 240
 GGAGGAGGCC CATGACTATG AGGTGGACAT CAATGGTTTA GAGATCCTTG AATGCAAATA 300
 CAGGGTGGCA GTAAGTGGAG TGATTGATCT GAAAGCTGAA ATTAAGGCCT TAAAGGAGAA 360
 ATATAATAAA TCTGTAGAAA ACTACACTGA TGAGAAGGCC AAGTATGAGA GTAAATCCA 420
 GATGTATGAT GAGCAGGTGA CAAGCCTTGA GAAGACCACC AAGGAGAGTG GTGAGAAGAT 480
 GGCCACATG GAGAAGGAGT TGCAAAAGAT GACCAGCATA GCCAACGAAA ATCACAGTAC 540
 CCTTAATACG 550

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Gln Val Glu Arg Glu Lys Ala Ile Leu Leu Ala Asn Leu Gln Glu
 1 5 10 15
 Ser Gln Thr Gln Leu Glu His Thr Lys Gly Ala Leu Thr Glu Gln His
 20 25 30
 Glu Arg Val His Arg Leu Thr Glu His Val Asn Ala Met Arg Gly Leu
 35 40 45
 Gln Ser Ser Lys Glu Leu Lys Ala Glu Leu Asp Gly Glu Lys Gly Arg

ATTY DOCKET NO.: GIN-6054CP

50	55	60
Asp Ser Gly Glu Glu Ala His Asp Tyr Glu Val Asp Ile Asn Gly Leu		
65	70	75 80
Glu Ile Leu Glu Cys Lys Tyr Arg Val Ala Val Thr Glu Val Ile Asp		
	85	90 95
Leu Lys Ala Glu Ile Lys Ala Leu Lys Glu Lys Tyr Asn Lys Ser Val		
	100	105 110
Glu Asn Tyr Thr Asp Glu Lys Ala Lys Tyr Glu Ser Lys Ile Gln Met		
	115	120 125
Tyr Asp Glu Gln Val Thr Ser Leu Glu Lys Thr Thr Lys Glu Ser Gly		
	130	135 140
Glu Lys Met Ala His Met Glu Lys Glu Leu Gln Lys Met Thr Ser Ile		
	145	150 155 160
Ala Asn Glu Asn His Ser Thr Leu Asn Thr		
	165	170

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCCATGAGT GAATTCATCC AAGGGCACGG GTTCAGCAAG GAAAAAAGGT TAACCGTGGT	60
TCCACCAGCA AAAAGAGATT GTCAGCAGCC TGTGCTTCCG TACCGCCACA GTGTTACACAA	120
CTAGCCGGGA GGCAAGACTG CCCAACTGTC AGTCCTGACA CAGCTCTCCC TGAGGAGCAG	180
CCACATTCCA GCTCCCAGTG CGCCCCTCTC CACTGTCTCT CCAAGCCTCC TCACCCCTAG	240
TCTTCATCTC CTGTGGACAA ACATCTGGGG TGGAAAGTTT GTAGCCACAC ACAGGATACT	300
GCCCAAGATC CAGCGGGTGT TTTCTTCTCG GTTGTTAGAT GTACAATTGG ATTAATGTCC	360
ATCGTTTTGG AAGACGAGAG AAAGTTGAGA AGAACACGAA GCACAGACCC TGATGTGATA	420
AAACATTTTG TGGTTTCTCT GAGTCACAGA TAAACTTCTG CCATCAAATG GCTACAGTTC	480
ATTTAAATTT AAAAAAAAAA AAAAA	505

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

ATTY DOCKET NO.: GIN-6054CP

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

GGATACTGTA ATAAATAGGA GACAGCTACA GTGATCCAAC TAAACCAACA GGGGATTTTC      60
ATCAGCACTT CCCTGGTGTA ATCATGGTAC AGATTATTAA AGACACGAAT GAATTTAAAA      120
CATTTTGTGAC AGCTGCCGGA CACAACTCG CAGTGGTTCA ATTTTCTTCG AAACGGTGTG      180
GTCCCTGCAA AAGGATGTTT CCTGTTTTCC ATGAGCTGGC TGAAACTTGT CACATCAAAA      240
CAATACCCAC ATTTAGATG TTCAAGAAAA GCCAGAAGGT AACCTATTC TCAAGAATCA      300
AAAGAATAAT TTGCTGTTAT AGAAGTGGAT TCATGAGCAA CCTGATTTTT GAGTTTTGTG      360
GAGCCGATGC TAAAAAATTG GAAGCCAAGA CTCAAGAATT AATGTAAGCT GATCTCCAAG      420
GCAAAATACA CTTGTGACAT TTGAAAAGGC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      480
A                                                                                   481

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(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Val Gln Ile Ile Lys Asp Thr Asn Glu Phe Lys Thr Phe Leu Thr
1           5           10           15
Ala Ala Gly His Lys Leu Ala Val Val Gln Phe Ser Ser Lys Arg Cys
20           25           30
Gly Pro Cys Lys Arg Met Phe Pro Val Phe His Glu Leu Ala Glu Thr
35           40           45
Cys His Ile Lys Thr Ile Pro Thr Phe Gln Met Phe Lys Lys Ser Gln
50           55           60
Lys Val Thr Leu Phe Ser Arg Ile Lys Arg Ile Ile Cys Cys Tyr Arg
65           70           75           80
Ser Gly Phe Met Ser Asn Leu Ile Phe Glu Phe Cys Gly Ala Asp Ala
85           90           95
Lys Lys Leu Glu Ala Lys Thr Gln Glu Leu Met
100           105

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

ATTY DOCKET NO.: GIN-6054CP

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCAAAGAG GCCTATTCCT GTGTGCAATC AGTACCTTGA AGGCAGAACA TTCTGAATAA	60
AGTTGGAAAA AGAACAGCTT TGCTTTGCAA AGATTGATGA CAGACTGGTT CCTCAGAGGC	120
CTAGGCTACC CGTCACCCCT TTTTCCAGAG CGAGGGCCTG GAATGAAGGC AGTTTATCCT	180
CTGTCCCTGG AGCCTGGGGT TTGCTTTGGC TCCTTGAGGT GGAAGAGACT AAGAGGGCAG	240
CTGCCCAGAG CAGCTGTGTG TACCTGGCTC CTCTCAGGCT TCCTGATCCC TTCCATTGCA	300
CTGCGCCTTA TCCCTCAGCC AGCCAGACAG CCTCCCTGCT CCTGACCAGC AGATACGTTT	360
CGGAGTGGTT GGTGTGGTTT TTGTGATGAG GGCAGCACGT GGTGGCCAAG GTGGCAAGCT	420
GAGTCTCACA GGCTCACTCC CTCGTTGGTT CCCTGTGGGA ATGGTAGGCC AGGCCARTA	480
AGCCATGCCC CAACACGTCC TCTCCTCCGG AGGAAGGGCC AGCTGCCARC TGARTCAGCA	540
GCTAGTCCAT AGCACAGCCT TATAACTGTA AAGCCAGGCA TTGCCCATGA GCAGAGCTGG	600
AACCAGAGCT TCAGTCAGTA AGAGGGAGGA TTACCTTCAG GAGAAGGCAA GGAAGAAAAC	660
TGGCTGCTAT CTTTATAGTT CCACTGCCCT AACCAAGTGT CCACATTCTA AATGTGTAGT	720
GTCCATCCCT TATGTAATAG TGGTTTCCCG CCCAAAGTGA GACTTTCCTT TTAATTGGAG	780
AAGGGTATAG AGGTAGTCCA GGTGGGAACG CCAGAAGTGC TGATTGCCCA GCCATTGGGA	840
CCACCTGTTC TTGCCCCACT ACCCTCTAGT GGGAGGCCAA AGTAAAGGCT GGCTGGTGGG	900
TGTCTGTGGA TTGAGGATGT GGCAGGGACT GGTCCCTCCA CCTCCCTCTG GCCAAAGATG	960
GGCTTTGCCC GCTGTGTGCC TGTCACCACC CACCAGCAGT CATGCCCTGG GCTTCCCAA	1020
TGGAGAGGTA GCAGGCAACG TTTTAAAAA GAAAGAAAAC AGGAAACTGT ATTGTGTCGG	1080
GGGAGGCGGG AGGGAGATGA GGAAACGGTT TGGATTTTGT GTGTGGGAGG GTATTTTTTG	1140
GGGGTAGTTG TCTGTAACCT TCCTAAGTGC TTTTTCCT TTTCTTTTTT AAAGTAAGTT	1200
GCAGGCTTTG GCTTGAAAAA CCCCAGGGGG ATGGGGGGCA GAAACCTGAG GCTGCTGCCC	1260
TTTATCTGCC TTCACGGTAC TGTCCCCTTC CCCCAGCTCC TCCCTGACCC CATGGGCCAG	1320
GCCTCAGACC TTCCAGCTAA CCGCTTCCA TGAGCCACTA CTCTGATGTC AGCCTATAAC	1380
CAAAGGAGCT GGGGGGTCCA GGCCTGGTGA CCAACCTTTC TCAGCCCACT CAATCAGGGT	1440
GCTCCCCACC TGCAGGCAGG AGGCAACACC CTATCTGCTA CCATCAGCCC CTTCCAGAGC	1500
CCATCTGCCC CGCCCAGCCC TGCCCTGCCC AGCCATACCC TGCTCTGCCC CATCTGGGGG	1560
TGCCCTGCTC AGGGATGGGC TGGCAGGGCT GTACCCAGCC TCCCTGGTAA GCAGAGACTC	1620
AAGAAACCTC TGGGGTCCTG TTTTCTGGTC GTGTGATCCC AGGGGTGCAC ATGGGCCCCCT	1680

TGGGTGTCTG AACAGAAGGG CATGGGAGGG AGGGCTGCAC CCCTGCAGTC TTACTCTGCT 1740
 GGTGTAGCGG GCAGMTGCCC ACTCCCACCC CACCCTGCAC CGCGGGCTCC TGAGTCGGCA 1800
 GATTAAGCAT TTTATAAATT GTATTTTAAA TACATGTTTT AAACCTGTCA AAAAAAAAAA 1860
 AAAA 1864

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Val Leu Pro Thr Cys Arg Gln Glu Ala Thr Pro Tyr Leu Leu Pro Ser
 1 5 10 15
 Ala Pro Ser Arg Ala His Leu Pro Arg Pro Ala Leu Pro Cys Pro Ala
 20 25 30
 Ile Pro Cys Ser Ala Pro Ser Gly Gly Ala Leu Leu Arg Asp Gly Leu
 35 40 45
 Ala Gly Leu Tyr Pro Ala Ser Leu Val Ser Arg Asp Ser Arg Asn Leu
 50 55 60
 Trp Gly Pro Val Phe Trp Ser Cys Asp Pro Arg Gly Ala His Gly Pro
 65 70 75 80
 Leu Gly Cys Leu Asn Arg Arg Ala Trp Glu Gly Gly Leu His Pro Cys
 85 90 95
 Ser Leu Thr Leu Leu Val
 100

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCCCTCGTA CTGATTTCCA TCGTTGCATT TACAACTGCT ACAAAAATGC CAGCACTCCA 60
 TCGACATGAA GAAGAGAAAT TCTTCTTAAA TGCCAAAGGC CAGAAAGAAA CTTTACCCAG 120
 CATATGGGAC TCACCTACCA AACAACTTTC TGTCGTTGTG CCTTCAAACA ATGAAGAAAA 180
 ACGGTTGCCT GTGATGATGG ATGAAGCTCT GAGCTATGTA GAGAAGAGAC AGAAACGAGA 240

TCCTGCGTTC ACTTATGAAG TGATAGTAGT TGATGATGGC AGTAAAGATC AGACCTCAAA 300
 GG TAGCTTTT AAATATTGCC AGAAATATGG AAGTGACAAA GTACGTGTGA TAACCCTGGT 360
 GAAGAATCGT GGAAAAGGTG GAGCGATTAG AATGGGTATA TTCAGTTCTC GAGGAGAAAA 420
 GATCCTTATG GCAGATGCTG ATGGAGCCAC AAAGTTTCCA GATGTTGAGA AATTAGAAAA 480
 GGGGCTAAAT GATCTACAGC CTTGGCCTAA TCAAATGGCT ATAGCATGTG GATCTCGAGC 540
 TCATTTAGAA AAAGAATCAA TTGCTCAGCG TTCTTACTTC CGTACTCTTC TCATGTATGG 600
 GTTCCACTTT CTGGTGTGGT TCCTTTGTGT CAAAGGAATC AGGGACACAC AGTGTGGGTT 660
 CAAATTATTT ACTCGAGAAG CAGCTTCACG GACGTTTTCA TCTCTACACG TTGAACGATG 720
 GGCATTTGAT GTAGAACTAC TGTACATAGC ACAGTTCTTT AAAATTCCAA TAGCAGAAAT 780
 TGCTGTCAAC TGGACAGAAA TTGAAGGTTT TAAATTAGTT CCATTCTGGA GCTGGCTACA 840
 AATGGGTAAA GACCTACTTT TTATACGACT TCGATATTTG ACTGGTGCCT GGAGGCTTGA 900
 GCAAACTCGG AAAATGAATT AGGTTGTTTG CAGTCTTCAG TTGTGTTCTT ATGCTTCAGT 960
 GTCACATTTT ATTTCAATTTG AAATAAAAT TTTAAGTAAA GCTGAAATAA ACTTCTTGTC 1020
 ATTGTCAAAA AAAAAAAAAA A 1041

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Pro Ala Leu His Arg His Glu Glu Glu Lys Phe Phe Leu Asn Ala
 1 5 10 15
 Lys Gly Gln Lys Glu Thr Leu Pro Ser Ile Trp Asp Ser Pro Thr Lys
 20 25 30
 Gln Leu Ser Val Val Val Pro Ser Asn Asn Glu Glu Lys Arg Leu Pro
 35 40 45
 Val Met Met Asp Glu Ala Leu Ser Tyr Val Glu Lys Arg Gln Lys Arg
 50 55 60
 Asp Pro Ala Phe Thr Tyr Glu Val Ile Val Val Asp Asp Gly Ser Lys
 65 70 75 80
 Asp Gln Thr Ser Lys Val Ala Phe Lys Tyr Cys Gln Lys Tyr Gly Ser
 85 90 95
 Asp Lys Val Arg Val Ile Thr Leu Val Lys Asn Arg Gly Lys Gly Gly
 100 105 110

Ala	Ile	Arg	Met	Gly	Ile	Phe	Ser	Ser	Arg	Gly	Glu	Lys	Ile	Leu	Met
		115					120					125			
Ala	Asp	Ala	Asp	Gly	Ala	Thr	Lys	Phe	Pro	Asp	Val	Glu	Lys	Leu	Glu
	130					135					140				
Lys	Gly	Leu	Asn	Asp	Leu	Gln	Pro	Trp	Pro	Asn	Gln	Met	Ala	Ile	Ala
145					150					155					160
Cys	Gly	Ser	Arg	Ala	His	Leu	Glu	Lys	Glu	Ser	Ile	Ala	Gln	Arg	Ser
				165					170					175	
Tyr	Phe	Arg	Thr	Leu	Leu	Met	Tyr	Gly	Phe	His	Phe	Leu	Val	Trp	Phe
			180					185					190		
Leu	Cys	Val	Lys	Gly	Ile	Arg	Asp	Thr	Gln	Cys	Gly	Phe	Lys	Leu	Phe
		195					200					205			
Thr	Arg	Glu	Ala	Ala	Ser	Arg	Thr	Phe	Ser	Ser	Leu	His	Val	Glu	Arg
	210					215					220				
Trp	Ala	Phe	Asp	Val	Glu	Leu	Leu	Tyr	Ile	Ala	Gln	Phe	Phe	Lys	Ile
225					230					235					240
Pro	Ile	Ala	Glu	Ile	Ala	Val	Asn	Trp	Thr	Glu	Ile	Glu	Gly	Ser	Lys
				245					250					255	
Leu	Val	Pro	Phe	Trp	Ser	Trp	Leu	Gln	Met	Gly	Lys	Asp	Leu	Leu	Phe
			260					265					270		
Ile	Arg	Leu	Arg	Tyr	Leu	Thr	Gly	Ala	Trp	Arg	Leu	Glu	Gln	Thr	Arg
	275						280					285			
Lys	Met	Asn													
	290														

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CNCCATCGGG GAACACCAGA AAGAACACT

29

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TNTCTGGCAT ATCCGTCAGG TTAAACTCC

29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CNCTGGTTCT ACATCAATAC CAGCTTTCC

29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TNACAACAGT GATATTTGAG AGCTTCAAG

29

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CNGTAACACC TCTCCAACGC TTTCGATGC

29

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GNCAAGGACA GACACGTGGA AATGAAGAC

29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ANGTCCACCT CATAGTCATG GGCCTCCTC

29

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TNTCAGCCAG CTCATGGAAA ACAGGAAAC

29

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CNTGGGAAGC GGTTAGCTGG AAGGTCTGA

29

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TNTCTTCTTC ATGTCGATGG AGTGCTGGC

29

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg Val Lys Val Gln Leu Ala Leu Val Phe Phe Lys Asn Leu Ala Ser
 1 5 10 15
 Ser Cys Thr Leu Asp Ser Ala Leu Asn Ala Ala Ser Tyr Tyr Asn Phe
 20 25 30
 Thr Val Leu Lys Val Pro Arg Ser Met Thr Asp Pro Gln Asn Met Glu
 35 40 45
 Phe Gln Val Pro Val Ile Leu Thr Ser Gln Ala Asn Ala Pro Leu Leu
 50 55 60
 Ala Gly Asn Thr Cys Gln Asn Val Val Ser Gln Val Thr Tyr Glu Ile
 65 70 75 80
 Glu Thr Asn Gly Thr Phe Gly Ile Gln Lys Val Ser Val Ser Leu Gly
 85 90 95
 Gln Thr Asn Leu Thr Val Glu Pro Gly Ala Ser Leu Gln Gln His Phe
 100 105 110
 Ile Leu Arg Phe Arg Ala Phe Gln Gln Ser Thr Ala Ala Ser Leu Thr
 115 120 125
 Ser Pro Arg Ser Gly Asn Pro Gly Tyr Ile Val Gly Lys Pro Leu Leu
 130 135 140
 Ala Leu Thr Asp Asp Ile Ser Tyr Ser Met Thr Leu Leu Gln Ser Gln
 145 150 155 160
 Gly Asn Gly Ser Cys Ser Val Lys Arg His Glu Val Gln Phe Gly Val
 165 170 175
 Asn Ala Ile Ser Gly Cys Lys Leu Arg Leu Lys Lys Ala Asp Cys Ser
 180 185 190
 His Leu Gln Gln Glu Ile Tyr Gln Thr Leu His Gly Arg Pro Arg Pro
 195 200 205
 Glu Tyr Val Ala Ile Phe Gly Asn Ala Asp Pro Ala Gln Lys Gly Gly
 210 215 220
 Trp Thr Arg Ile Leu Asn Arg His Cys Ser Ile Ser Ala Ile Asn Cys
 225 230 235 240
 Thr Ser Cys Cys Leu Ile Pro Val Ser Leu Glu Ile Gln Val Leu Trp

	245		250		255
Ala Tyr Val Gly Leu Leu Ser Asn Pro Gln Ala His Val Ser Gly Val	260		265		270
Arg Phe Leu Tyr Gln Cys Gln Ser Ile Gln Asp Ser Gln Gln Val Thr	275		280		285
Glu Val Ser Leu Thr Thr Leu Val Asn Phe Val Asp Ile Thr Gln Lys	290		295		300
Pro Gln Pro Pro Arg Gly Gln Pro Lys Met Asp Trp Lys Trp Pro Phe	305		310		315
Asp Phe Phe Pro Phe Lys Val Ala Phe Ser Arg Gly Val Phe Ser Gln	325		330		335
Lys Cys Ser Val Ser Pro Ile Leu Ile Leu Cys Leu Leu Glu Leu Gly	340		345		350
Val Leu Asn Leu Glu Thr Met	355				

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTTGTACCAT TCTTGCCAAC TTCTGGGCTG GCAGTATGGA GTCATCTCCC TATCTTTCAT	60
TGCCTGTGTG AAATCTACTT TCTGAATTCT GCCATTTCCC TCTTCACACT GTCTCCTGGG	120
TTATCTTTGC TTCCTCACAT CCCTATCTCT CTTCTATAA ACTGGCTCCC GTCACATTCCA	180
TGATCCCTTC AGTGGCTTCT GAGCTGGTCT CCCTGACCCC AAAGCCTCAG CCTTCCAGTC	240
TCCCTACAAA ATCTCAGCAA GTTCATTTTA GGTTAAAATT TGGACATATT TTAAATACGG	300
CTCACCACTT CATGTGAAAA TGATGGCACC CTACCAAGCA GTTTGCAGAG TTACGGTAAC	360
TGTTTCATGC TAATGATGTT ATTCATCCAG TTACAATTTT CTCAAACTC CTTTGGGCAC	420
TCTTTATTTT TAATCAAATT TTAAAGCCAA TATTTTCAATT TGAGAATATG AATTAAATTG	480
GGAAATTCAT CCTTGTGGTA CAGTTTACAG ATTTTAAATG TTTACCCATT TATCCTGTTT	540
TTTGATATAT TAATTTCCCA TATAGCTCCA GAGTTATGTG ATATTATTTT TTTGCCAGTA	600
TATTAGAAAA TGATTAATTT CTCATGACCA ACTTCTGAAA AGAAAGACCC AATGCAAAAT	660
GCAATCTATT ACAATTATTT TTTTGAATAA AAAAGAATAT ATTATAGTTC TTTAACATTT	720
GATATTTTAA ATTTGACATA TTCTTGATAT TTGTAAGAAA TTTCCACTGA ATGAATTTTA	780

ATTY DOCKET NO.: GIN-6054CP

CACAATTCAG ATACTACCAA TTAACATAATT CTAGCCTAAA CAAATAACAT TATTTTTTAAA	840
TAACAAAATC TTTAAAAATA ATTTTCTATT TTGAACCTTT AGCCATAATG TAAGAAAATA	900
AAATTTTCTA GCAGAATAAT CAAAGAGTGA AACAAAGTTC CAACATGTTT TTTCTTTGCA	960
ATTAAACATG GCACTTTTAC AGTTATTTAT TATTCATATC AGTGCACTTA CCGACTTCAT	1020
ATTTTCAAAT CAAAATACAG TGTTTTTCTC CAGTGAAATC CTTATTCTCA TGA CTGATAG	1080
AAAACATTGC CAATTTTGAT ATTTCCAGAG TTAATGTTAA ATTATTTGAA AGAAAATTAT	1140
TTAAAATAAT AAAAATAGAC ATTTCAAGAC TATTTCTTAT CACATAATTC AAAAAGTACT	1200
TGGATCAAAT CCTACAGAGT TTCTCCACTA AAATTCTACT TGTGCAGAGG GCATTGAAAC	1260
GCATGAAAAT CAACAGCAGC TTAGTTAGGT TAATTAATTC GGTTAATTAA GCACCTACTA	1320
CATGCTCAGC TCTATGCTAG GTGTCATGAG GAATTTAAAAG GACATGTAAT GCACATTTTC	1380
TGATTTCAAG GAGCTTTAAA TATTATTGTG TAGAAAAAGT TAACATCTAT GAAAATAGAA	1440
GTGGGGCAAT TTTGTGCTTA ATTCCATGGT CCAGATACAT CAAAAAATCA ATGTGGGCTG	1500
TCAAAGAAGG TTTCTTGATA GTCATGAGTC AGCCTGATTC TTGAAAGGAT ATGTGGAATA	1560
TAAATTTTAA TTTATATTCC TTTTGAGAAA ATACTGAGAA AACCATCTTC CCTGGAAAAG	1620
AGAACGTATT GTAAAGAAAG TACATGAAAT TGAAGGTTGA ATATCCAACA TCCCCCACAC	1680
TGCCCCAGTG TCTCTGCTCC CTTACTGAGC CTTACTATTA TTCTTCATAG CCCTATCACT	1740
ACCTAGTCTA GTATTCCTG AACTGTGTCA TCCACTAGAA TATGAGCATA ATGAGAGCAG	1800
AGACTACACC TGTCGGTTCA GTATTCTATC CTCAGCACAT AGAATGGTAC CTGGCACATA	1860
GCAGATGCTA AAATAAAATT TAAATGAATA AATTAATTCA ATCAACAAC TCAAGGTGTT	1920
ATTATTACCT ACAACTATTG TTTACAAGAG GTATGCACCG TGGAAGATCC TGGAGACACA	1980
ACAATGAATA AAGCCAAGCC AGTTCCTGCC CCCGTGGAGC TTGTAGTCAA GACATTGAAC	2040
AAGTGATCAG AAAGATGTTG ACTGCTGCAG CAGAGGGTTG CAAGCTGCTC ATGAGTATAT	2100
AACAAGTAGC CCTAACCAAA GCATTCTCTC CCTTGGTTTA ATGTCCACCC ATTGAGGTGA	2160
CTGCTAAATA CTAATCCATG ACTCTATCCC TTGGCATTCA AACTCACACA TCCACTTACC	2220
TGCCTCTCCA ACCTCATCTC CCTCCACTCA CAAGAGCCCA TCATATTATT CATCAAAATG	2280
AAACTGCACC CAGTTCTTCT GAACATATTA CCTTACAAAA CTTTCATTTA TGCCTGGTGA	2340
CTCTCATCAG GCATTCAAAA GCTTTCCCTC AGTGCTTCAG GGCTCTTCCT TTTCTTCCCT	2400
TTATACATAC ACCTTTATGT ATCTTCATAC GTACCCTGCA TAACCTCATA TATCTTAGCA	2460
TTTACCATAT TCTGTTGAAA AACTGTTTCC ATTTCTCTTT ACTTACTAGA ATGTAAACAG	2520
ATGCACAATG TTGAGAAAAT GAAAAGTGAC AACTTTGTTT ACAAGTTTAG AAATTATCAG	2580
ATTCTCACYT AAGCTCTAGT CTCTGTAAAG TCCACAAC TA CTYAATAAAA GTGAAGAAAA	2640

ATGTTAACAG AGAGGGAGGA ATCAAAAACA AAGAACTATT TAAAAA AAAA

2696

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

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Met Thr Leu Ser Leu Gly Ile Gln Thr His Thr Ser Thr Tyr Leu Pro
1           5           10           15

Leu Gln Pro His Leu Pro Pro Leu Thr Arg Ala His His Ile Ile His
20           25           30

Gln Asn Glu Thr Ala Pro Ser Ser Ser Glu His Ile Thr Leu Gln Asn
35           40           45

Phe His Leu Cys Leu Val Thr Leu Ile Arg His Ser Lys Ala Phe Pro
50           55           60

Gln Cys Phe Arg Ala Leu Pro Phe Leu Pro Phe Ile His Thr Pro Leu
65           70           75           80

Cys Ile Phe Ile Arg Thr Leu His Asn Leu Ile Tyr Leu Ser Ile Tyr
85           90           95

His Ile Leu Leu Lys Asn Cys Phe His Phe Ser Leu Leu Thr Arg Met
100          105          110

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(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

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CGCGCTAACT GTGCTCCTCC GGGGCCCTCC GCCTGCTCCC AGCCATGGTG GCCTGGCGCT      60
CGGCGTTTCCT TGTCTGCCTC GCTTTCTCCT TGGCCACCCT GGTCCAGCGA GGATCTGGGG      120
ACTTTGATGA TTTTAACCTG GAGGATGCAG TGAAAGAAAC TTCCTCAGTA AAGCGATCAC      180
TGTAAGGATG ACATGGGAGG AGCCATGTGA AGCACTCAGC ACAGTCCTTG GAACAAGAGC      240
CATGGGACCA CACCACCACC ACCACAACCA ATAGGCCAGG AACCACCAGA GCTCCGGCAA      300
AACCTCCAGG TAGTGGATTG GACTTGGCTG ATGCTTTGGA TGATCAAGAT GATGGCCGCA      360
GGAAACCGGG TATAGGAGGA AGAGAGAGAT GGAACCATGT AACCACCACG ACCAAGAGGC      420

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CAGTAACCAC CAGAGCTCCA GCAAATACTT TAGGAAATGA TTTTGACTTG GCTGATGCCC	480
TGGATGATCG AAATGATCGA GATGATGGCC GCAGGAAACC AATTGCTGGA GGAGGAGGTT	540
TTTCAGACAA GGATCTTGAA GACATAGTAG GGGGTGGAGA ATACAAACCT GACAAGGGTA	600
AAGGTGATGG CCGGTACGGC AGCAATGACG ACCCTGGATC TGGCATGGTG GCAGAGCCTG	660
GCACCATTGC CGGGGTGGCC AGCGCCCTGG CCATGGCCCT CATCGGTGCC GTCTCCAGCT	720
ACATCTCCTA CCAGCAGAAG AAGTTCTGCT TCAGCATTCA GCAGGGTCTC AACGCAGACT	780
ACGTGAAGGG AGAGAACCTG GAAGCCGTGG TATGTGAGGA ACCCCAAGTG AAATACTCCA	840
CGTTGCACAC GCAGTCTGCA GAGCCGCCGC CGCCGCCCGA ACCAGCCCGG ATCTGAGGGC	900
CCTGTCCAGC TGCAGGCATG CACAATGGTG CCACCGCTTG TCACCCGGCT CCCCCACCC	960
CTTCATTTGG ACCCGCAGCT GCTGTGCTGC TCTGTGCCGT CGGCTCCTTG TTGGTCTGAG	1020
TTTCCCGGAT GAGCTCTGGG TGTTTGTGAG TTTGGTTTCT CTGCCCTGCC CCAAGCGTGC	1080
TGAGACTTGG TGCCGAAATT CAAGAGCCAG CTCTGATAGA AAGCCAGCAC CAGCCTCGGG	1140
AGCTGCTGAG CCACCAACTC CCAAAGCCAG CCTGCCTCCA GCTTTACTGA GCACAGGATG	1200
CGGGGGCCAA GATGATGCTG AGGCCTGATG ACATTTATGC TTAGGGGACA AGAGTTTGAA	1260
CTCAAGGGAC TGTGACCCCT GCACACTGGA GTGGCTCATT GTGGCAGGTT TCTGCCAATA	1320
GACAGCCCCT GACAGTGGCC TCAAGGAGCT GCAGGTGGGG GGCTCAGCCT GCACCCACTT	1380
GGAGCCCCTG CAAGGAGCGA ACCGGTCAGC ACCAAGTAAC ACCACACACA CGCAGCACCC	1440
AGGATGATGG TTCACTTCA GTCTTCCCCA TCCCAGGTTT TATGTTGCTG GGCTTCCGGA	1500
GAGCCGGTCC AAGCGGAGGC TTTCAGTGAT TTAAGTACAA ACATGCATCT CGTGATAGTC	1560
CTGCCTTGAG AGCTTAGGAA TCTTCCGGAT AAGTATGAAG CAATTCGTAG GCCTGTTTCC	1620
CATCTGATTC CATAGGGGGC TGGGTGTGGC TTCGGGTTGA CATGAGAAAG GTCTTTAGCA	1680
ATCATTTCTG CACCGGAGAT GAGTTTATC CTGTGTTGGG GAGAGGTGCT CACCCTCCAC	1740
CCTGTGTCCC TGTTTTGGTA GCAAGAGTGA CCGATGTCAA GAACGAGCAT CAAAGCCAGA	1800
ATCCTGCTTG TTTGCTTAAA AATGTAATTG GGGGCGGCGG GGGAGGAGAG GGGAAAGAGA	1860
CATTGCTTG GTTTAGTGAA ACGCAGGTGA CTTTGTAGCT CTGTGGTCAG CCTACTTGTC	1920
TGCTCTGAGG GAGAGTGCCT GGGGAGCCAT GCTCACCCTG GCAAACACAG GAACCCCATG	1980
ACTCGCCCCT CACCTGGCGT GGAGCTGCCT GGTTCGGGCT GGAGCAGAGC TGGTTTCCTG	2040
GAATGTTCTT TTGGCCCACA TATGGTTCTG TCCCGGTGAG CTCTGTTGTC AGAGGCTCAC	2100
GGGACAGAAC CACATGCTAG GGTCTAGGGC CCCTGTCTAC TGATAGTCAG TTTGCTGTGT	2160
CAGAAAGCAC TTCTGAAAGC AGATATGAGT CACCAGACAG GCAGGATCTT ACAAACCTCA	2220

ATTY DOCKET NO.: GIN-6054CP

CGGGCCTCTT TGGTCTGCAT GATGGCCCCA TCGTTCAT AGGCTGTCCA CTGAGCGGGA	2280
TTGTCTGCTG AGTGGGATGA GCCAACTCCA GTTCTTAAG GAAACCACTG GAATCTGCAG	2340
CCCCACATG CATCTGTCTA ACGCATGCCT CGTGTTTCGTT TTGCAAACAT GCCTGTGGTG	2400
GAGGGTGGTC AGTTGTAGCC CTGTGCGTCT CAAGGCTGCC TTGTGAGGCC ATTCCCAGTG	2460
CGTGCCCTTG AGCTCCTTAC CACCCCTTTT CCTGCTCGGC CCTTTAATCC CTGACAGACC	2520
TGGACTGTGT GGCTGAAGGG GGACCTGCAG CACTGCAGAA ATGCCTCTGC GTGGTGCCAT	2580
GAAGGAAAGA AACCTTGGCC TGGTCTCGAG AAGCTTCCCA TGCTTCAGGA AGTTAGTAAG	2640
GGTGGGGTGG CTTGCAGGAT TGGCCTGTTT CCAGGGCCTC CCACACTCAT TGGCCAGATT	2700
GTGAACTTTG TCAGGCTTGT CCCTCCCTGA TACCAAGTAT GTCGAGAACC GATGGCCCCA	2760
CCCTCTGGCT GGTGCTGGGC CGGAGGTGGC TATGGAGGAT TTTGGCATGC GTGGCCTGTC	2820
GCCACCTGGA CAGCGTGACC TCAGGGGTTG TCCACTTTAC CTTTATGGTG AGGCCTGTGC	2880
GATGGCTAAG TCCTTGAAAC CCTAGAGCTG TGACGTAGAA TATGTGCTGT CTGTGAGACC	2940
GTGTTCCCAG GAGCACTGAC TGCAGTTGAG AGAGACCCAT TTTGCTCTCC CTTACCGCCC	3000
CCCGCCCCGG GTGCTTTCTG CACAAAGCCT AGAGCCTGGC ACTCAAGCCC ACCGGTGGCA	3060
GCTCCTAGTG ACTGGACATG CCTGGAAGAC CCCTCAGCCT TCTGTTTGCA GAACGTTTAT	3120
TTCAGGAGCT TCTCCTTCCC ACAGACATCT TACACTTGCT CGACACTGCC ACCTGCAGAA	3180
GCCTGGCGGG CTCTGGTCAC CATGTGTCTA TCTGAAGGTT GCACTGGCCA GCATGGGCCT	3240
GTCCCAAGCG AGAGGGGAGA CACAGTGGAC TGAAAGGACT GGTTGAAAGT GGCCAATCTC	3300
TGTCAGCTTA ATTTGGCAGA GAAAATTTGT AACAACTCTG AGCACATGCT GGGTGAAGTC	3360
ACAGCTCAAG GAAAGATAAA GCTGGGCGGA AGGAGGTGTG CGTGGCTTCT GGGGTGGGAC	3420
CCAGAGGGGA GGCTCTGGGA CAGGGGCTGG GGTTCAGTGC CAGGGCCCTG AGGAAGAAAT	3480
GGGGACTGAT CTCAAAATTC CAGAATTCCC TGTACATCTG TTCACGTGCT TGTGTCCAGG	3540
TGTGACTTGT AAAGTGTCTA GTGTTTGCAT TAAATAAAAT GGCACCGAGC AAAAAAAAAA	3600
AAAAAAAAAA AAAA	3614

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Val Lys His Ser Ala Gln Ser Leu Glu Gln Glu Pro Trp Asp His Thr

(2) INFORMATION FOR SEQ ID NO:39:

(A) LENGTH: 1077 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

-29-

CGAATCGACG TCGTCACGTG ACGGTCTGCC TCCGCCCTTA TTAAGTCTCA GCCCAGCGGC	240
GGTTTCCAGG ACCTCAGACT TTTTGCCGAG GCGGCAGTCC CTAGACGAAG CGAAGGAGGC	300
GGCGCCTGCC CCGCCCACAA GAGCTGCCGC GCGCGGGTGT TATAGCTCCA CCCCATCTGC	360
AAAGGAAGGG GGAGCGGAAA GAGCGGGATC TAGCGTGGGA TAAAAGTGGG ACTACTACAG	420
TGTAAGTGGG CATGCGCCCC TCCTAGAAAT GATGGGAATG CAAAAGCCCT TGACTGCTCC	480
AGGACTCGAG GGATCCTCGG TGCCAGGATG CTGGGTCAAG CGCTCCGCCG GGACAGAGGA	540
CTCATACCAG GGAAATGGAG CCCAGCCTCG TGATAAACTA CGACCCAAGC TGGGGGAGGA	600
ACCTAGTTTT CGAAAGGAAA ATAATATGCG CAAGCTTTAA CTGAGCAGTG GGATGGTCTT	660
AAATACCAAA GGAATGACTT TAAATCTTGC TGGATGGGAC TGCCACTCAC CGCTAGAAAT	720
CGGGGATCAA CAGCAAACTC TGGATGACCC TGTAACCACA TCTCCAGTTC AGCCCGGCGA	780
GGGGCATCCT CACCCACCAG CAAAGTACCA TCCACCTTAT TGATGACAGG GATCCGGGTC	840
TCCAGGTCCA CATCAAGGTG ATTAGGCTCT TCCATGCACT CCACCTCCAG CTGCAAACCC	900
AGAATCCACC CCCATGAGCA CATACTCTTC TTTGGGGGAG GGAGGGAGGG GGAGCAGGGC	960
CAATGGTAGT CATGAAATGA CTCTAGTATT TTCCATTCCC CCAGTCCCAC TGCCTTCATC	1020
AATTATTGGG AATAAAAAGA CAATCTAATC GTCAAAAAAA AAAAAAAAAA AAAAAAA	1077

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Asp	Gly	Gly	Lys	Arg	Glu	Arg	Lys	Thr	Arg	Glu	Asn	Gln	Gln	Asn
1				5					10					15	
Val	Arg	Cys	Lys	Glu	Ser	Ile	Phe	Ala	Gly	Phe	Val	Asn	Phe	Ala	Thr
			20					25					30		
Ala	Ala	Arg	Glu	Ser	Thr	Ser	Ser	Arg	Asp	Gly	Leu	Pro	Pro	Pro	Leu
			35					40				45			
Leu	Thr	Leu	Ser	Pro	Ala	Ala	Val	Ser	Arg	Thr	Ser	Asp	Phe	Leu	Pro
			50			55					60				
Arg	Arg	Gln	Ser	Leu	Asp	Glu	Ala	Lys	Glu	Ala	Ala	Pro	Ala	Pro	Pro
65					70				75					80	
Thr	Arg	Ala	Ala	Ala	Arg	Gly	Cys	Tyr	Ser	Ser	Thr	Pro	Ser	Ala	Lys
				85					90					95	

Glu Gly Gly Ala Glu Arg Ala Gly Ser Ser Val Gly
100 105

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TAAGAATTAA AAATGTCATC CAAACAAGAA ATAATGAGTG ACCAGCGGTT TAGACGGGTT	60
GCAAAGGACC CGAGATTTTG GGAAATGCCA GAAAAGGATC GAAAAGTCAA AATTGACAAG	120
AGATTTTCGAG CCATGTTTCA TGACAAGAAG TTCAAGTTGA ACTATGCCGT GGATAAAAGA	180
GGGCGCCCCA TTAGCCATAG CACTACAGAG GATTTGAAGC GTTTTACGA CCTTTCAGAT	240
TCTGATTCCA ATCTCTCTGG TGAAGATAGC AAAGCATTGA GTCAAAAGAA AATAAAGAAG	300
AAAAAAACCC AGACTAAAAA AGAAATCGAT TCAAAAAATC TAGTTGAGAA AAAGAAAGAA	360
ACCAAGAAGG CTAATCACAA GGGTTCTGAA AATAAACTG ATTTAGATAA TTCTATAGGA	420
ATTAAAAAAA TGAAAACCTC ATGTAAATTT AAGATAGATT CAAACATAAG TCCGAAGAAG	480
GATAGCAAAG AATTTACACA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	540
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA	588

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ser Ser Lys Gln Glu Ile Met Ser Asp Gln Arg Phe Arg Arg Val	
1 5 10 15	
Ala Lys Asp Pro Arg Phe Trp Glu Met Pro Glu Lys Asp Arg Lys Val	
20 25 30	
Lys Ile Asp Lys Arg Phe Arg Ala Met Phe His Asp Lys Lys Phe Lys	
35 40 45	
Leu Asn Tyr Ala Val Asp Lys Arg Gly Arg Pro Ile Ser His Ser Thr	
50 55 60	
Thr Glu Asp Leu Lys Arg Phe Tyr Asp Leu Ser Asp Ser Asp Ser Asn	
65 70 75 80	

Leu Ser Gly Glu Asp Ser Lys Ala Leu Ser Gln Lys Lys Ile Lys Lys
85 90 95
Lys Lys Thr Gln Thr Lys Lys Glu Ile Asp Ser Lys Asn Leu Val Glu
100 105 110
Lys Lys Lys Glu Thr Lys Lys Ala Asn His Lys Gly Ser Glu Asn Lys
115 120 125
Thr Asp Leu Asp Asn Ser Ile Gly Ile Lys Lys Met Lys Thr Ser Cys
130 135 140
Lys Phe Lys Ile Asp Ser Asn Ile Ser Pro Lys Lys Asp Ser Lys Glu
145 150 155 160
Phe Thr Gln

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTATATTTTG GTTTACTTAC TCCTCTATTT CAGAAATTGA AAAAGATCCC CAAGGATCTG	60
TTACTACTGC ATTTCCCTTCT TGCTCTGTCT ACAGCCTAGG CCAACTAGTC AGGGTCTGGA	120
CATGCATCTC CTAAAGGAAG AACTGTGTAG CACCATTGAT CACAATGTAA CATTTCATG	180
CTGCATTAAG GGTGTCTCTC TCTAATCATG ATTGTACCTG TCTCTTCCTG GGTAAGGGA	240
GATTTTTTTT TTTAATGTG TAAAGAATTG ATGCSAGCCA GGAACATGTC TGTAGTCCCA	300
GCTACTTGGG CACACGCCTG TAGTCCMSCG CCACTCGAGC ACACACCTGT AGTACCAGCT	360
ACTCTGGAGG CTGAGGCAGG AGGATCACTT GAGCCCAGGA GATTAAGACT GTAGTATACT	420
ATGATCGTGC CTGTGGCTAG CCACTGTGCT CCAGCCTGGG CAACACCATC GTAAAAATAA	480
ATAAATAAAT AAATAAATTG GGGAGGACAG CCTCACTGGT ATCAGACTTA CAGGACCAGA	540
TAGACAAGAT GGGTATAAGG GGAGCTGAAG TCTGTGTTCA TATGAGGAAG AGAAGACCAA	600
GCCCTGGGAC TTTGGCTGAA TTCCTCCGTG GGGCTGGACG GCAGTGATCT CCTGTTCCCT	660
ATGTGTAAAC AAAGATTCCA GGGCGTGGTT TTGCACTCCT GTTGTACTCT TTTAGAGGTG	720
GAAAAGAGGT GGATACTGAG ATCTAAGAGG AAAGGATAGT CATTACGTT CTGAGATATG	780
CGCTCTCTCT ATTGTTCTCG WACACAAAGG GATAGTCTCT TTTCTGGAGC TGATGTCCCT	840
GCTTGAGGT TAGCCCCAAA ACATGGCTCT TGTATTGTTT TAAGAGAAAA GGCTTTCATT	900

TTGGTTCTTC TGATTGGTGT TACCTACTGC CTAATATGTG TTCATTTTTT GACAGAGAGG	960
CAGACTATTG AAAAAGTCTG TGTGAACAGA GAGCAGTTCA TTAAGCCCAT TGCTTTCAGT	1020
AATGTGGCCT TGACCCCTTC TGCTTCCCC TTCTCCCATG GAGCATGGCA GGGCTTGTT	1080
ATTTAGAGTC CATACTGCA AGCCATTGAG AGACTTGTTT GCTCAAATGC AAGTTTGCTC	1140
AAAAACAGGT CCTGAAGGCT TGCTTAGGAT TACAGGGATG CTGGGTAAGA ACACCGTTCC	1200
TCTCTCTCGC TGGAGAAATC CCTGTTTCTC TGACTCCCTT TGTGATCCTC ACAGTAATGT	1260
ATTCTGTGCC ACTGTAGGAC ACAAGGCTCT GGGCCAGTAG AACAGGCAGA GAGGTGACAC	1320
TGGGCAGCAA GCTGAGAGCT CTTTCTAAAT GGAGTGAAGG AATTCAGTGG CCTAGTTTCG	1380
CCATTCTCTA ATGAGAAACC AAGGCCAGGC TGAAAAGTGC AATTAGATGT GGTGGATTGT	1440
GGTAACGGCC TCCAGATAAA GGGGTTATCC CTGTGGAAGT GACTTTTCCC CATTTGATCC	1500
CTTTTCAACT CTAAATGGCC AGGCCAGAG CAGAAGAAGG GTTGGGTCTG GAAGGAAGGC	1560
TCCAAAGGAT GAAAGCTTCT CCCTGATCAT AAGGAAGTGC ATCTTTATAG AATTGTTGTG	1620
CATAATGTCA GTAAATCCCT CTCACCTGAC AAGGGACTGG ATTCATCTTG CCTTGAGACG	1680
GGCCAGTAGT TATCAGTGAG TCAAAGCAAA GTGAAAGTTT CAGGAGATGG GACCAATGGT	1740
GCAATGCTCG CCATAACAAA ATTCCTTAAA AATAAAAAAG CTAATGTTAT AGCAACAAAA	1800
AAAGACTGAA GCAAACCAC ACTGAAATGC ATCCCACTCC AGGAGAGGAA TTCTTAGCGT	1860
AACACTCTAA ATAAATGGAA GGAATCATCA CCTTCCTTAT TTTACCCCTG CCTTGTTTAC	1920
CAGGCTGCCC AGTGCTTACC ATGCAGAAAG CAGTCAGCTG TACTCTGGAA GTTCTGTTC	1980
TTCTTTCCTG GGGCTTAGGA TATTCTGGGA GCTGTCTGAG CCTTGTGCCT AAGGCTTATC	2040
AGGTGATATA ATCTTCCTGT TCTGGGCTGC TTGCTGGAGG AATAGGAAGT GACATTTATA	2100
AGACACAGGC GGTGTGAGCA TCCATGTGTG GTCTTGGTCT AAACCAGCTC TTGAACAGGT	2160
TAAAGCAAAC AGCAATAACA AAACAAAAAC TACTGATGCT GAGCGTTTTG ATCCTAGTAA	2220
TATTTCAAAT ATTGTCCTTC TGCATATGTT CTATCCATAT TTGATTCAA TATACATTAT	2280
TAAGCTTCT TGGGTACTAT TTTGCTGGG CTCTTGCCTG AAGGTGGTAC CTGTCTCATG	2340
ATCCTTAAAA GAGAGAGGCT TTTTTCATCC AAAGCTGTAG TGTTGGGAAC TGGGGTGGGA	2400
GAGGCACTTT TTGGAATTCT GAAAGAATCA TATCTGTGTA TATACATACT GAGTGGGGAA	2460
GGATGGGGGT TGGCAGGGGT TGAGGGAGGT GGGAACAAAC AGTGAGTATG GGAACAGGCA	2520
GTCACCTCGA GTGTGGGAGG TCACCTGGGT CCGTCGTCTT CCTTCTGTAT GGTGTTGGGT	2580
TTATGTACAC ACTATAACAC TTCCTGTGTG AGTTCATGTA CCTGTCTGTG AGTGCTTTGG	2640
TGTATTGAGC CTCAGTACAC TCCAAGGGCA TTAAAGTCAA GAACTAGAAC CTGGAAAAAA	2700
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2760

AAAAAAAAAA AAA

2773

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Met Arg Ser Leu Tyr Cys Ser Arg Thr Gln Arg Asp Ser Leu Phe Ser
 1             5             10             15
Gly Ala Asp Val Pro Ala Trp Arg Leu Ala Pro Lys His Gly Ser Cys
          20             25             30
Ile Val Leu Arg Glu Lys Ala Phe Ile Leu Val Leu Leu Ile Gly Val
          35             40             45
Thr Tyr Cys Leu Ile Cys Val His Phe Leu Thr Glu Arg Gln Thr Ile
          50             55             60
Glu Lys Val Cys Val Asn Arg Glu Gln Phe Ile Lys Pro Ile Ala Phe
          65             70             75             80
Ser Asn Val Ala Leu Thr Pro Ser Ala Ser Pro Phe Ser His Gly Ala
          85             90             95
Trp Gln Gly Leu Val Ile
          100

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

GGAAACATTA TGGATCTGTG GAGCTGCTTA TTTCCAGTGA TGCTGATGGA GCCATCCAAA      60
GGGCTGGAAG ATTCAGAGTG GAAAATGGCT CTTAGATGA GAATGCAACT GCCCTGCCTG      120
GTACTTGGCG AAGAACAGAC GTGCACTTAG AGAACCCAGA ATACCACACC AGATGGTATT      180
TCAAATATTT TTTAGGACAA GTCCATCAGA ACTACATTGG AAACGATGCC GAGAAGAGCC      240
CTTTCTTCTT GTCCGTGACC CTTTCTGACC AAAACAATCA ACGTGTCCCT CAATACCGTG      300
CAATTCTTTG GAGAAAAACA GGTACCCAGA AAATATGCCT TCCCTACAGT CCCACAAAAA      360
CTCTTTCTGT GAAGTCCATC TTAAGTGCCA TGAATCTGGA CAAATTTGAG AAAGGCCCCA      420

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GGGAAATTTT TCATCCTGAA ATACAAAAGG ACTTGCTGGT TCTTGAAGAA CAAGAGGGCT	480
CTGTGAATTT CAAGTTTGGG GTTCTTTTTG CCAAAGATGG GCAGCTCACT GATGATGAGA	540
TGTTCAGCAA TGAAATTGGA AGCGAGCCTT TTCAAAAATT TTTAAATCTT CTGGGTGACA	600
CAATCACTCT AAAGGGCTGG ACGGGCTACC GTGGCGGTCT GGATACCAAA AATGATACCA	660
CAGGGATACA TTCAGTTTAT ACTGTGTACC AAGGGCATGA GATCATGTTT CATGTTTCCA	720
CCATGTTGCC ATATTCCAAA GAGAACAAAC AGCAGGTGGA AAGGAAACGC CACATTGGAA	780
ACGATATCGT CACCATTTGTG TTCCAAGAAG GAGAGGAATC TTCTCCTGCC TTTAAGCCTT	840
CCATGATCCG CTCCCCTTT ACACATATTT TTGCCTTAGT GAGATACAAT CAACAAAATG	900
ACAATTACAG GCTGAAAATA TTTTCAGAAG AGAGCGTACC ACTCTTTGGC CCTCCCTTGC	960
CAACTCCACC AGTGTTTACA GACCACCAGG AATTCAGGGA CTTTTTGCTA GTGAAATTAA	1020
TTAATGGTGA AAAAGCCACT TTGGAAACCC CAACATTTGC CCAGAAACGT CGGCGTACCC	1080
TGGATATGTT GATTAGATCT TTACACCAGG ATTTGATGCC AGATTTGCAT AAGAACATGC	1140
TTAATAGACG ATCTTTTAGT GATGTCTTAC CAGAGTCACC CAAGTCAGCG CGGAAGAAAG	1200
AGGAGGCCCCG CCAGGCGGAG TTTGTTAGAA TAGGGCAGGC ACTAAACTG AAATCCATTG	1260
TGAGAGGGGA TGCTCCATCA AGCTTGGCAG CTTCAGGGAT CTGTAAAAA GAGATGACCT	1320
TCCATCAGTG CCCGTGTTTG ACAGAACTCT GCCAGTGAAG CAAATGCATG TGCTTGAGAC	1380
CCTGGACCTT CTGGTTCTCA GAGCAGACAA AGGAAAAGAT GCTCGCCTCT TTGTCTTCAG	1440
GCTAAGTGCT CTGCAAAAGG GCCTTGAGGG GAAGCAGGCT GGGAAGAGCA GGTCTGACTG	1500
CAGAGAAAAC AAGTTGGAGA AAACAAAAGG CTGCCACCTG TATGCTATTA AACTCACCA	1560
CAGCAGAGAG CTGAGGATTG TGGTTGCAAT TCGGAATAAA CTGCTTCTGA TCACAAGAAA	1620
ACACAACAAG CCAAGCGGGG TCACCAGCAC CTCATTGTTA TCTCCCCTGT CTGAGTCACC	1680
TGTTGAAGAA TTCCAGTACA TCAGGGAGAT CTGTCTGTCT GACTCTCCCA TGGTGATGAC	1740
CTTAGTGGAT GGGCCAGCTG AAGAGAGTGA CAATCTCATC TGTGTGGCTT ATCGACACCA	1800
ATTTGATGTG GTGAATGAGA GCACAGGAGA AGCCTTCAGG CTGCACCACG TGGAGGCCAA	1860
CAGGGTTAAT TTTGTTGCAG CTATTGATGT GTACGAAGAT GGAGAAGCTG GTTTGCTGTT	1920
GTGTTACAAC TACAGTTGCA TCTATAAAAA GGTTCGCCCC TTTAATGGTG GCTCTTTTTT	1980
GGTTCAACCT TCTGCGTCAG ATTTCCAGTT CTGTTGGAAC CAGGCTCCCT ATGCAATTGT	2040
CTGTGCTTTC CCGTATCTCC TGGCCTTCAC CACCGACTCC ATGGAGATCC GCCTGGTGGT	2100
GAACGGGAAC CTGGTCCACA CTGCAGTCGT GCCGCAGCTG CAGCTGGTGG CCTCCAGGTC	2160
GGATATATAC TTCACAGCAA CTGCAGCTGT GAATGAGGTC TCATCTGGAG GCAGCTCCAA	2220

GGGGGCCAGT GCCCGAAATT CTCCTCAGAC ACCCCCGGGC CGAGATACTC CAGTATTTCC 2280
 TTCTTCCCTG GGGGAAGGTG AAATTCAATC AAAAAATCTG TACAAGATTC CACTTAGAAA 2340
 CCTCGTGGGC AGAAGCATCG AACGACCTCT GAAGTCACCC TTAGTCTCCA AGGTCATCAC 2400
 CCCACCCACT CCCATCAGTG TGGGCCTTGC TGCCATTCCA GTCACGCACT CCTTGTCCCT 2460
 GTCTCGCATG GAGATCAAAG AAATAGCAAG CAGGACCCGC AGGGAACACT TGGGCCTCTC 2520
 GGATGAAGGT GGACCCAAGT CAGAAGGAGC GCCAAAGGCC AAATCAAAAC CCCGGAAGCG 2580
 GTTAGAAGAA AGCCAAGGAG GCCCCAAGCC AGGGGCAGTG AGGTCATCTA GCAGTGACAG 2640
 GATCCCATCA GGCTCCTTGG AAAGTGCTTC TACTTCCGAA GCCAACCCCTG AGGGGCACTC 2700
 AGCCAGCTCT GACCAGGACC CTGTGGCAGA CAGAGAGGGC AGCCCGGTCT CCGGCAGCAG 2760
 CCCCTTCCAG CTCACGGCTT TCTCCGATGA AGACATTATA GACTTGAAGT AACAGAGTTG 2820
 AATCTCATTT GCCATCTTTA GTTTTCTTAT GGAGGTTTAT ACTCTTTAAA CAGTTCTGAT 2880
 GTAATTTCTC AACAAAATGT GGCTTTTAGC CTGTCAGTGA TCTATTGGAC CAAACCTTCT 2940
 GCACACTCGG CCAGTTCCTT CTCCAATGTC CGGTGCCATC TTTCTGACC TTTGTTTCTT 3000
 TCTGTTTCTC AACCATCAGT CCCCTTGTA TAAAGGTGGT AGATTTCATT GAGGTTTTAG 3060
 ATTGAACTT TGAATAAATC AAAAATACTC ATTCTTAAAA AAAAAAAAAA AAAAAAAAAA 3119

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Asn Leu Asp Lys Phe Glu Lys Gly Pro Arg Glu Ile Phe His Pro
 1 5 10 15
 Glu Ile Gln Lys Asp Leu Leu Val Leu Glu Glu Gln Glu Gly Ser Val
 20 25 30
 Asn Phe Lys Phe Gly Val Leu Phe Ala Lys Asp Gly Gln Leu Thr Asp
 35 40 45
 Asp Glu Met Phe Ser Asn Glu Ile Gly Ser Glu Pro Phe Gln Lys Phe
 50 55 60
 Leu Asn Leu Leu Gly Asp Thr Ile Thr Leu Lys Gly Trp Thr Gly Tyr
 65 70 75 80
 Arg Gly Gly Leu Asp Thr Lys Asn Asp Thr Gly Ile His Ser Val
 85 90 95
 Tyr Thr Val Tyr Gln Gly His Glu Ile Met Phe His Val Ser Thr Met

100	105	110
Leu Pro Tyr Ser Lys Glu Asn Lys Gln Gln Val Glu Arg Lys Arg His		
115	120	125
Ile Gly Asn Asp Ile Val Thr Ile Val Phe Gln Glu Gly Glu Glu Ser		
130	135	140
Ser Pro Ala Phe Lys Pro Ser Met Ile Arg Ser His Phe Thr His Ile		
145	150	155
Phe Ala Leu Val Arg Tyr Asn Gln Gln Asn Asp Asn Tyr Arg Leu Lys		
165	170	175
Ile Phe Ser Glu Glu Ser Val Pro Leu Phe Gly Pro Pro Leu Pro Thr		
180	185	190
Pro Pro Val Phe Thr Asp His Gln Glu Phe Arg Asp Phe Leu Leu Val		
195	200	205
Lys Leu Ile Asn Gly Glu Lys Ala Thr Leu Glu Thr Pro Thr Phe Ala		
210	215	220
Gln Lys Arg Arg Arg Thr Leu Asp Met Leu Ile Arg Ser Leu His Gln		
225	230	235
Asp Leu Met Pro Asp Leu His Lys Asn Met Leu Asn Arg Arg Ser Phe		
245	250	255
Ser Asp Val Leu Pro Glu Ser Pro Lys Ser Ala Arg Lys Lys Glu Glu		
260	265	270
Ala Arg Gln Ala Glu Phe Val Arg Ile Gly Gln Ala Leu Lys Leu Lys		
275	280	285
Ser Ile Val Arg Gly Asp Ala Pro Ser Ser Leu Ala Ala Ser Gly Ile		
290	295	300
Cys Lys Lys Glu Met Thr Phe His Gln Cys Pro Cys Leu Thr Glu Leu		
305	310	315
		320
Cys Gln		

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1592 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GACTTTTATA AAAAAGTCAA GCAGTACAAA AGGGTGTAAA GTGAAGTTAC TGTCTTCCC	60
CTCCATAAAC CCCCTGACCT TGGGAACTG TTGTTAACAG TTAAGTGGT AACTTTTCAG	120
ATATTTTGTA TGCATGTACA AATGTGAGTA TCTAATGTAA AAAAATCAAA CCAAGATAAA	180

GTGTAAACTG CTATGATGGA ATCCTGCCTT GTTCTGCTAT TAGTCTTCTG TTTAATAATC 240
AGCTTTGGTA TTAGGACAGT GGTAGGAAGA AGCCAGTATG TCCTGCAACA TAATTTGTGG 300
TTCTGGACTG GTCAGGATTT CCTGAATGCA GCCTTTATCT GGAAGCTCTG CCCTTCTCCA 360
TCTGGGATAC GCTTTTTTCAT CCATCAAAAC TGTCATCTCC CTCTGTGAAG CCTTCCCTGA 420
CTATTCTCTG TCCCTCTTTC CTCTCTTCCC ACAAACACAA CTGTGTACGC GTGTCACCAA 480
AGAGTTAATC GTGCTTTTCT CTGTGCTACT TTTATACSTA GTATATGGTC CATTGTTTTG 540
CACTTAATAC ACTCTCTTGT AATGATTTGT TTACATGTCA GTCTCCCAGC CAGACTGAGA 600
GCTCACCAAG GGCAGAAGCC GTGTTTTGTT TACTGCTGTA TTCCTGGTAC CTGGTACAAT 660
GCTTGGCATA CAGTTGGATG AACGGGAAAG TAATCTGAGC TGCCGGTGCT GTGGCAGTGC 720
AAAGTGGGCA TATTTGTGCC CTTGGACCAG ATGTAGCCCT TGATGCATTT TGCAGGAACA 780
CGGCTTAGTT ATTGTTTACT TTGAAGCCCT TTTGCCTCTA CTCTCTCCCA TATATCTTCT 840
CCTGACAGGG TGAAGTCACC TATAGCATTT CCTAGTGTAT GGAAGTATTA ATTTCTTTCT 900
TTRACTGGAAG AGCTACTAGC TTTTCTTCAT ACAGTTTCCT CTGCTCCAGT TTCATAAGTT 960
TCTTTTTTGGC TTGTATCTGT TTAGGATCAG GTGATATGGC TTCATTTCTC ATGACTGAAG 1020
CCCGGCAACA TAACACTGAA ATTCGAATGG CAGTCAGCAA AGTGGCTGAT AAAATGGATC 1080
ATCTCATGAC TAAGGTTGAA GAGTTACAGA AACATAGTGC TGGCAATTCC ATGCTTATTC 1140
CTAGCATGTC AGTTACAATG GAAACAAGCA TGATTATGAG CAACATCCAG CGAATCATTC 1200
AGGCCAAGGT GACAGAGGAG TTAGCAGCGG CCACTGCACA GKTCTCTCAT CTGCAGCTGA 1260
AAATGACTTG CTCACCAAAA AAAGGAAACA GAGCTGCAGA TGCAGCTGAC AGAAAGCCTG 1320
AAGGAGACAG ATCTTCTCAG GGGCCAGCTC ACCAAAGTGC AGGCAAAGCT CTCAGAGCTC 1380
CAAGAAACYT CTGAGCAAGC ACAGTCCAAA TTCAAAAGTG AAAAGCAGAA CCGGAAACAA 1440
CTGGAActCA AGGTGACATC CCTGGAGGAG GAACTGACTG ACCTTCGAGT TGAGAAGGAG 1500
TCCTTGGAAG AGGTAAGCTC TACAACCCAG TTTGCCAGAA TTAGCTGTTT AATAAACATT 1560
TTTATTTTCC TTTTACAAAA AAAAAAAAAA AA 1592

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Glu Val Leu Ile Ser Phe Phe Thr Gly Arg Ala Thr Ser Phe Ser

1	5	10	15
Ser Tyr Ser Phe Leu Cys Ser Ser Phe Ile Ser Phe Phe Leu Ala Cys	20	25	30
Ile Cys Leu Gly Ser Gly Asp Met Ala Ser Phe Leu Met Thr Glu Ala	35	40	45
Arg Gln His Asn Thr Glu Ile Arg Met Ala Val Ser Lys Val Ala Asp	50	55	60
Lys Met Asp His Leu Met Thr Lys Val Glu Glu Leu Gln Lys His Ser	65	70	75
Ala Gly Asn Ser Met Leu Ile Pro Ser Met Ser Val Thr Met Glu Thr	85	90	95
Ser Met Ile Met Ser Asn Ile Gln Arg Ile Ile Gln Ala Lys Val Thr	100	105	110
Glu Glu Leu Ala Ala Ala Thr Ala Gln Xaa Ser His Leu Gln Leu Lys	115	120	125
Met Thr Cys Ser Pro Lys Lys Gly Asn Arg Ala Ala Asp Ala Ala Asp	130	135	140
Arg Lys Pro Glu Gly Asp Arg Ser Ser Gln Gly Pro Ala His Gln Ser	145	150	155
Ala Gly Lys Ala Leu Arg Ala Pro Arg Asn Xaa	165	170	

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGGAAACGGG AAGCCGCTGC AAGTCCACCG CCTCAGCTAC CCAGATTGGG ATCTGCCCAG	60
GCCCGCTTTA TGGACTAGTG TGGGCGGCAG GCTCCTTTCC GTCCCTGCCC TGCTGTACCC	120
CGCTCCTTGG AGACCCCTG TATCCCTCCC GCAAGGTGGA ATCCGCAGGC TGGAGGCTCC	180
CAGGGGAGGC AAACGCCTGG CCCTGCCCTG CCCCACGCCG CACCATGACC CTCCTGCTGC	240
TGCCCTTCT GCTGGCCTCT CTGCTCGCGT CCTGCTCCTG TAACAAAGCC AACAAGCACA	300
AGCCATGGAT TGAGGCAGAG TACCAGGGCA TCGTCATGGA GAATGACAAC ACGGTCCTAC	360
TGAATCCACC ACTCTTTGCC TTGGACAAGG ATGCCCCGCT GCGCTATGCA GGTGAGATCT	420
GCGGCTTCCG GCTCCATGGG TCTGGGGTGC CCTTTGAGGC TGTGATCCTT GACAAGGCGA	480
CAGGAGAGGG GCTGATCCGG GCCAAGGAGC CTGTGGACTG CGAGGCCAG AAGGAACACA	540

CCTTCACCAT CCAGGCCTAT GACTGTGGCG AGGGCCCCGA CGGGGCCAAC ACCAAGAAGT 600
 CCCACAAGGC CACTGTGCAT GTGCGGGTCA ACGATGTGAA CGAGTTTGCC CCAGTGTGTTG 660
 TGGAACGGCT GTATCGTGCG GCTGTGACAG AGGGGAAGCT GTACGATCGC ATCCTGCGGG 720
 TGGAAGCCAT TGACGGTGAC TGCTCCCCC AGTACAGCCA GATCTGCTAC TATGAGATTC 780
 TCACACCCAA CACCCCTTTC CTCATTGACA ATGACGGGAA CATTGAGAAC ACAGAGAAGC 840
 TGCAGTACAG TGGTGAGAGG CTCTATAAGT TTACAGTGAC AGCTTATGAC TGTGGGAAGA 900
 AGCGGGCAGC AGATGATGCT GAGGTGGAGA TTCAGGTGAA GCCCACCTGT AAACCCAGCT 960
 GGCAAGGCTG GAACAAAAGG ATCGAATATG CACCAGGTGC TGGGAGCTTG GCTTTGTTCC 1020
 CTGGTATCCG CCTGGAGACC TGTGATGAAC CACTCTGGAA CATTGAGGCC ACCATAGAGC 1080
 TGCAGACCAG CCATGTGGCC AAGGGCTGTG ACCGTGACAA CTACTCAGAG CGGGCGCTGC 1140
 GGAAACTCTG TGGTGCTGCC ACTGGGGAGG TGGATCTGTT GCCCATGCCT GGCCCCAATG 1200
 CCAACTGGAC AGCAGGACTC TCGGTGCACT ACAGCCAGGA CAGCAGCCTG ATCTACTGGT 1260
 TCAATGGCAC CCAGGCTGTG CAGGTGCCCC TGGGTGGCCC CAGTGGGCTG GGCTCTGGGC 1320
 CCCAGGACAG CCTCAGTGAC CACTTCACCC TGTCTTCTG GATGAAGCAT GGCGTAACTC 1380
 CCAACAAGGG CAAGAAGGAA GAGGAAACCA TCGTATGTAA CACTGTCCAG AATGGTGAGC 1440
 CTCCCCTCCA GGCCTAGCC AGAGGGGGAA ACTGGCTTCT TGTCCCGCCT CTGTCACTGC 1500
 CCAGTGTGTG ACTGTGAACA GGTCACTTCC CCTCTCTTCA TTTGTGAGGT GCAAGTGCCA 1560
 GGTGTGATAT GCCTTGATTC TGTGCTTTAT CCCCAACATG ACATGTTGGA TCGTAAAAAA 1620
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1680
 AAAAAAAAAA AAAA 1694

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Thr Leu Leu Leu Leu Pro Leu Leu Leu Ala Ser Leu Leu Ala Ser
 1 5 10 15
 Cys Ser Cys Asn Lys Ala Asn Lys His Lys Pro Trp Ile Glu Ala Glu
 20 25 30
 Tyr Gln Gly Ile Val Met Glu Asn Asp Asn Thr Val Leu Leu Asn Pro
 35 40 45

Pro Leu Phe Ala Leu Asp Lys Asp Ala Pro Leu Arg Tyr Ala Gly Glu
50 55 60

Ile Cys Gly Phe Arg Leu His Gly Ser Gly Val Pro Phe Glu Ala Val
65 70 75 80

Ile Leu Asp Lys Ala Thr Gly Glu Gly Leu Ile Arg Ala Lys Glu Pro
85 90 95

Val Asp Cys Glu Ala Gln Lys Glu His Thr Phe Thr Ile Gln Ala Tyr
100 105 110

Asp Cys Gly Glu Gly Pro Asp Gly Ala Asn Thr Lys Lys Ser His Lys
115 120 125

Ala Thr Val His Val Arg Val Asn Asp Val Asn Glu Phe Ala Pro Val
130 135 140

Phe Val Glu Arg Leu Tyr Arg Ala Ala Val Thr Glu Gly Lys Leu Tyr
145 150 155 160

Asp Arg Ile Leu Arg Val Glu Ala Ile Asp Gly Asp Cys Ser Pro Gln
165 170 175

Tyr Ser Gln Ile Cys Tyr Tyr Glu Ile Leu Thr Pro Asn Thr Pro Phe
180 185 190

Leu Ile Asp Asn Asp Gly Asn Ile Glu Asn Thr Glu Lys Leu Gln Tyr
195 200 205

Ser Gly Glu Arg Leu Tyr Lys Phe Thr Val Thr Ala Tyr Asp Cys Gly
210 215 220

Lys Lys Arg Ala Ala Asp Asp Ala Glu Val Glu Ile Gln Val Lys Pro
225 230 235 240

Thr Cys Lys Pro Ser Trp Gln Gly Trp Asn Lys Arg Ile Glu Tyr Ala
245 250 255

Pro Gly Ala Gly Ser Leu Ala Leu Phe Pro Gly Ile Arg Leu Glu Thr
260 265 270

Cys Asp Glu Pro Leu Trp Asn Ile Gln Ala Thr Ile Glu Leu Gln Thr
275 280 285

Ser His Val Ala Lys Gly Cys Asp Arg Asp Asn Tyr Ser Glu Arg Ala
290 295 300

Leu Arg Lys Leu Cys Gly Ala Ala Thr Gly Glu Val Asp Leu Leu Pro
305 310 315 320

Met Pro Gly Pro Asn Ala Asn Trp Thr Ala Gly Leu Ser Val His Tyr
325 330 335

Ser Gln Asp Ser Ser Leu Ile Tyr Trp Phe Asn Gly Thr Gln Ala Val
340 345 350

Gln Val Pro Leu Gly Gly Pro Ser Gly Leu Gly Ser Gly Pro Gln Asp
355 360 365

Ser Leu Ser Asp His Phe Thr Leu Ser Phe Trp Met Lys His Gly Val
 370 375 380

Thr Pro Asn Lys Gly Lys Lys Glu Glu Glu Thr Ile Val Cys Asn Thr
 385 390 395 400

Val Gln Asn Gly Glu Pro Pro Leu Gln Ala Leu Ala Arg Gly Gly Asn
 405 410 415

Trp Leu Leu Val Pro Pro Leu Ser Leu Pro Ser Val
 420 425

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTGGTCCTCC TTTGCAGAGG TGGTGCGGAG CTCCTGTTTG ACGGTATTAA GAAACATCGA 60

GTCACCTTTGC CTGGACAGGA GGAACCCTGG GACATCCGGA ACCTGCTCAT CTGGATCAAG 120

AAGAATTTGC TAAAAGAGCG GCCAGAGTTG TTCATCCAGG GAGACAGCGT GCGGCCAGGA 180

ATTCTGGTGC TGATTAACGA TGCCGACTGG GAGCTACTGG GTGAGCTGGA CTACCAGCTT 240

CAGGACCAGG ACAGCGTCCT CTTTCATCTCC ACTCTGCACG GCGGCTGAGG GCCCTTCTCT 300

GGGCTTGGGC ACCCTTAGAG GGGAGAACGA AGCAATCAGA CATCCCCTTG GGCCCTGCTT 360

CCAGGTCTCC CTGTCCCCCT TGCCTGCCTT CTTCCCTGCT CTGTCCCCTA AGCTCCCTCC 420

AGGCAGGGAA AAGAGGCCAG GTGCTAAAAA TGAGCCTTTC TCAAGCACGT GAGCAGCGGA 480

AGGCAGACAG GCGCCAGAGC CCAGCACTCC CTTTTCCAGC AGCTGTGGTG GGGGAGGGTT 540

CCCCTCCAGT TTGTCAAGAG TTGAAGGAGG CTCTGTGGCC AGGTGACCTG GCTGCCTTCC 600

ACTCCTTGTA CCTCAGTCTA AACATGGAGT GGCCGCTGAC AAGGCGCTCC AGCCCCAGAG 660

CCAGCGTCTT CATGGGGAAG ATGAATGGAC CTGAGTAGCT GAAGGAAGGC CCCTCCCTAC 720

CCAAAGACTG GAGGCTTCTC AGCCTCAATT TCCCTGTCTG TACAGCTGAG GGCTCTGCCT 780

GTCCCCCACT GCTATCAGTA TGGAACCCCA GCTGGGGTCC CCTATTGAGT GCCGACTCCC 840

CCCACGCCA GCAGCTGCTC CTCCAGCCAC ACCCTTCCTG CTCCCCCCAC CCYTAGCCCT 900

TGACCCTGGC TGGCCTGCCC CGCTCCACAG GCCACCAGAT GGGCTCCTGA GACCCTCCCC 960

AGGCTGCTTA CAGCTCATTC TGCTGGGGGT AGAGATGAGG GGAGGGAGTA AGTTAAACCT 1020

TGGACTAGCA AGTAGAAGCC TGGGGGGATG CGTGTGCCTC AGTTTCCTC TCCACAACCTG 1080

AATATAGTGG CTGAAAACTG GGGAGATACT TGATGGCGCG AATGTCCGTT TTCTCTCCCT 1140

TCCCACCTCC TGCAGGAAGC AGGACGGGGC AGGCAGCACC TGGTAGGCAC AGTGCTTTGC 1200
 CCCTCCTCCC CTTCCCTTCT GGAAGTCTTG GGGCCTCAGT GCTTGCAACA GCCGGCCTTG 1260
 GGCAAATAAA AGACTAGGTT GTTTACTAAA AAAAAAAAAA AAAAAAAAAA 1309

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Ala Arg Met Ser Val Phe Ser Pro Phe Pro Pro Pro Ala Gly Ser
 1 5 10 15
 Arg Thr Gly Gln Ala Ala Pro Gly Arg His Ser Ala Leu Pro Leu Leu
 20 25 30
 Pro Phe Pro Ser Gly Ser Leu Gly Ala Ser Val Leu Ala Thr Ala Gly
 35 40 45
 Leu Gly Gln Ile Lys Asp
 50

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1740 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCCCGTGCG CTCCATCAAC CACGCCAGCC TCATCTCTGC ACTCTCCCGG GACTATCGCA 60
 ACCTGAAGCC CAGTGCTGTT GCCCCACAGA GAAAGATGCC ACTGGATGAC ACCAAACTGA 120
 TTATCCACCA GAACTCAGC GTCTTAGAAG ATATTGTGGA GAATATCTCG GGGGAGTCCA 180
 CCAAGTCTCG ACAGATTTGC TACCAGTCGC TGCAGGAATC TGTTCAAGTC TCCCTGGCCC 240
 TCTTTCCAGC TTTTATCCAT CAGTCAGATG TGAATGATGA GATGCTGAGC TTCTTCCTCA 300
 CTCTGTTTTG AGGCCTTAGA GTACAGATGG GTGTGCCTTT CACTGAGCAA ATCATAACAGA 360
 CTTTCCTCAA CATGTTTACC AGAGAGCAGT TAGCCGAGAG CATCCTCCAC GAGGGCAGCA 420
 CAGGCTGCCG GGTGGTGGAG AAGTTTCTGA AGATCCTGCA GGTGGTGGTC CAGGAGCCAG 480
 GCCAGGTGTT CAAGCCCTTC CTCCCAGCA TCATCGCCCT GTGCATGGAG CAAGTGTATC 540

CCATCATTGC CGAGCGTCCC TCCCCTGATG TGAAGGCCGA GCTGTTTGAG CTCCTTTTCC 600
 GGACGCTCCA TCACAAGTGG AGGTACTTCT TCAAGTCCAC CGTGCTGGCC AGTGTCCAGA 660
 GGGGGATCGC TGAGGAGCAG ATGGAGAATG AGCCCCAGTT CAGTGCCATC ATGCAGGCTT 720
 TCGGACAGTC CTTTCTCCAG CCCGACATCC ACCTTTTTTAA ACAAATCTC TTCTACTTGG 780
 AGACTCTCAA CACCAAGCAG AAGCTGTACC ACAAGAAGAT CTTCCGGAAT GCCATGCTGT 840
 TCCAGTTTGT GAACGTGCTG CTCCAGGTCC TGGTCCACAA GTCCCATGAT CTTCTGCAGG 900
 AGGAGATTGG CATCGCCATC TACAACATGG CCTCAGTCGA CTTTGATGGC TTCTTTGCCG 960
 CCTTCCTCCC AGAGTTCCTG ACCAGCTGTG ATGGTGTGGA TGCCAACCAG AAAAGTGTGC 1020
 TGGGGCGGAA TTTCAAGATG GATCGGGACC TGCCCTCATT CACCCAGAAT GTGCACAGGC 1080
 TGGTCAACGA CCTGCGCTAC TACAGACTCT GCAACGACAG CCTGCCCCCT GGCAGTGTGA 1140
 AGCTCTAGGC CTGCTACTGC CTGGGGACAC GGAATTCTGC TGCTGCCACC TGCGCCAGCC 1200
 CTACCTTCCA CCACAGATGT CTCCCAGATG GGCCTTGGTC AACTCCTTG GCTTCTCCCA 1260
 CCGCAAGCAA CGCTGCCTGC CTCTGCCGCT CCTCCACATC TTGCCGCTGC CCAGCAGAGC 1320
 TGGCTTCTGG GTCCACCTGA GCACTGGACG GTGCTCCCAG GGCCTTGGAG CAGGCGGAGG 1380
 GGTGTGTGGC CAGGTACTAG GAGGCACCAG GAAATCCCGC GGGGTGGCCC ATGCAGACCA 1440
 GCGGCACGTG GTCATGGGG CAGAATTGCC AAGGACAGCT CACGACAGTG CMACTTCTC 1500
 ACCATTCCAG CCAAGGAGAG ATGTGACGTT GGAAMTGYTY TGGCAMTTYT GTCAAGCCTC 1560
 CCGCGCCCCA ATTGCCTTGA RATYTYTGCT CTTTGTGAGA GATTTGCAA GACTCAMGTT 1620
 TTTGTTGTTT TCTCATCATT CCATTGTGAT ACTAAGAAAC TAAGAAGCTT AATGAAAAGA 1680
 AATAAAATGC CTATGTTGTT GTTCTAGGRR AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1740

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Pro	Leu	Asp	Asp	Thr	Lys	Leu	Ile	Ile	His	Gln	Thr	Leu	Ser	Val
1				5					10					15	
Leu	Glu	Asp	Ile	Val	Glu	Asn	Ile	Ser	Gly	Glu	Ser	Thr	Lys	Ser	Arg
		20					25						30		
Gln	Ile	Cys	Tyr	Gln	Ser	Leu	Gln	Glu	Ser	Val	Gln	Val	Ser	Leu	Ala
		35					40					45			

Leu Phe Pro Ala Phe Ile His Gln Ser Asp Val Thr Asp Glu Met Leu
 50 55 60
 Ser Phe Phe Leu Thr Leu Phe Arg Gly Leu Arg Val Gln Met Gly Val
 65 70 75 80
 Pro Phe Thr Glu Gln Ile Ile Gln Thr Phe Leu Asn Met Phe Thr Arg
 85 90 95
 Glu Gln Leu Ala Glu Ser Ile Leu His Glu Gly Ser Thr Gly Cys Arg
 100 105 110
 Val Val Glu Lys Phe Leu Lys Ile Leu Gln Val Val Val Gln Glu Pro
 115 120 125
 Gly Gln Val Phe Lys Pro Phe Leu Pro Ser Ile Ile Ala Leu Cys Met
 130 135 140
 Glu Gln Val Tyr Pro Ile Ile Ala Glu Arg Pro Ser Pro Asp Val Lys
 145 150 155 160
 Ala Glu Leu Phe Glu Leu Leu Phe Arg Thr Leu His His Asn Trp Arg
 165 170 175
 Tyr Phe Phe Lys Ser Thr Val Leu Ala Ser Val Gln Arg Gly Ile Ala
 180 185 190
 Glu Glu Gln Met Glu Asn Glu Pro Gln Phe Ser Ala Ile Met Gln Ala
 195 200 205
 Phe Gly Gln Ser Phe Leu Gln Pro Asp Ile His Leu Phe Lys Gln Asn
 210 215 220
 Leu Phe Tyr Leu Glu Thr Leu Asn Thr Lys Gln Lys Leu Tyr His Lys
 225 230 235 240
 Lys Ile Phe Arg Thr Ala Met Leu Phe Gln Phe Val Asn Val Leu Leu
 245 250 255
 Gln Val Leu Val His Lys Ser His Asp Leu Leu Gln Glu Glu Ile Gly
 260 265 270
 Ile Ala Ile Tyr Asn Met Ala Ser Val Asp Phe Asp Gly Phe Phe Ala
 275 280 285
 Ala Phe Leu Pro Glu Phe Leu Thr Ser Cys Asp Gly Val Asp Ala Asn
 290 295 300
 Gln Lys Ser Val Leu Gly Arg Asn Phe Lys Met Asp Arg Asp Leu Pro
 305 310 315 320
 Ser Phe Thr Gln Asn Val His Arg Leu Val Asn Asp Leu Arg Tyr Tyr
 325 330 335
 Arg Leu Cys Asn Asp Ser Leu Pro Pro Gly Thr Val Lys Leu
 340 345 350

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ANTGTCTTGA CTACAAGCTC CACGGGGGC

29

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TNGCCAAGGA GAAAGCGAGG CAGACAAGG

29

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ANATCGACTC TTTGCATCGC ACATTTTGT

29

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CNTTCTTCGG ACTTATGTTT GAATCTATC

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CNTTCCTCTT AGATCTCAGT ATCCACCTC

29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CNCAGACAGG GGAGATAACA ATGAGGTGC

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TNCTATAGGT GACTTCACCC TGTCAGGAG

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TNTTACAGGA GCAGGACGCG AGCAGAGAG

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ANTCAGTTGT GGAGGAGGAA ACTGAGGCA

29

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CNTCGAAACA GAGTGAGGAA GAAGCTCAG

29

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met	Val	Ala	Trp	Arg	Ser	Ala	Phe	Leu	Val	Cys	Leu	Ala	Phe	Ser	Leu
1				5				10					15		

Ala	Thr	Leu	Val	Gln	Arg	Gly	Ser	Gly	Asp	Phe	Asp	Asp	Phe	Asn	Leu
		20						25					30		

Glu	Asp	Ala	Val	Lys	Glu	Thr	Ser	Ser	Val	Lys	Gln	Pro	Trp	Asp	His
		35					40					45			

Thr	Thr	Thr	Thr	Thr	Thr	Asn	Arg	Pro	Gly	Thr	Thr	Arg	Ala	Pro	Ala
		50				55					60				

Lys	Pro	Pro	Gly	Ser	Gly	Leu	Asp	Leu	Ala	Asp	Ala	Leu	Asp	Asp	Gln
65				70					75						80

Asp	Asp	Gly	Arg	Arg	Lys	Pro	Gly	Ile	Gly	Gly	Arg	Glu	Arg	Trp	Asn
			85					90						95	

His	Val	Thr	Thr	Thr	Thr	Lys	Arg	Pro	Val	Thr	Thr	Arg	Ala	Pro	Ala
			100					105					110		

Asn	Thr	Leu	Gly	Asn	Asp	Phe	Asp	Leu	Ala	Asp	Ala	Leu	Asp	Asp	Arg
		115					120					125			

Asn	Asp	Arg	Asp	Asp	Gly	Arg	Arg	Lys	Pro	Ile	Ala	Gly	Gly	Gly	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130	135	140
Phe Ser Asp Lys Asp Leu Glu Asp Ile Val Gly Gly Gly Glu Tyr Lys		
145	150	155 160
Pro Asp Lys Gly Lys Gly Asp Gly Arg Tyr Gly Ser Asn Asp Asp Pro		
	165	170 175
Gly Ser Gly Met Val Ala Glu Pro Gly Thr Ile Ala Gly Val Ala Ser		
	180	185 190
Ala Leu Ala Met Ala Leu Ile Gly Ala Val Ser Ser Tyr Ile Ser Tyr		
	195	200 205
Gln Gln Lys Lys Phe Cys Phe Ser Ile Gln Gln Gly Leu Asn Ala Asp		
	210	215 220
Tyr Val Lys Gly Glu Asn Leu Glu Ala Val Val Cys Glu Glu Pro Gln		
	225	230 235 240
Val Lys Tyr Ser Thr Leu His Thr Gln Ser Ala Glu Pro Pro Pro Pro		
	245	250 255
Pro Glu Pro Ala Arg Ile		
	260	

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met His Val Leu Glu Thr Leu Asp Leu Leu Val Leu Arg Ala Asp Lys		
1	5	10 15
Gly Lys Asp Ala Arg Leu Phe Val Phe Arg Leu Ser Ala Leu Gln Lys		
	20	25 30
Gly Leu Glu Gly Lys Gln Ala Gly Lys Ser Arg Ser Asp Cys Arg Glu		
	35	40 45
Asn Lys Leu Glu Lys Thr Lys Gly Cys His Leu Tyr Ala Ile Asn Thr		
	50	55 60
His His Ser Arg Glu Leu Arg Ile Val Val Ala Ile Arg Asn Lys Leu		
	65	70 75 80
Leu Leu Ile Thr Arg Lys His Asn Lys Pro Ser Gly Val Thr Ser Thr		
	85	90 95
Ser Leu Leu Ser Pro Leu Ser Glu Ser Pro Val Glu Glu Phe Gln Tyr		
	100	105 110
Ile Arg Glu Ile Cys Leu Ser Asp Ser Pro Met Val Met Thr Leu Val		
	115	120 125

Asp Gly Pro Ala Glu Glu Ser Asp Asn Leu Ile Cys Val Ala Tyr Arg
 130 135 140
 His Gln Phe Asp Val Val Asn Glu Ser Thr Gly Glu Ala Phe Arg Leu
 145 150 155 160
 His His Val Glu Ala Asn Arg Val Asn Phe Val Ala Ala Ile Asp Val
 165 170 175
 Tyr Glu Asp Gly Glu Ala Gly Leu Leu Leu Cys Tyr Asn Tyr Ser Cys
 180 185 190
 Ile Tyr Lys Lys Val Cys Pro Phe Asn Gly Gly Ser Phe Leu Val Gln
 195 200 205
 Pro Ser Ala Ser Asp Phe Gln Phe Cys Trp Asn Gln Ala Pro Tyr Ala
 210 215 220
 Ile Val Cys Ala Phe Pro Tyr Leu Leu Ala Phe Thr Thr Asp Ser Met
 225 230 235 240
 Glu Ile Arg Leu Val Val Asn Gly Asn Leu Val His Thr Ala Val Val
 245 250 255
 Pro Gln Leu Gln Leu Val Ala Ser Arg Ser Asp Ile Tyr Phe Thr Ala
 260 265 270
 Thr Ala Ala Val Asn Glu Val Ser Ser Gly Gly Ser Ser Lys Gly Ala
 275 280 285
 Ser Ala Arg Asn Ser Pro Gln Thr Pro Pro Gly Arg Asp Thr Pro Val
 290 295 300
 Phe Pro Ser Ser Leu Gly Glu Gly Glu Ile Gln Ser Lys Asn Leu Tyr
 305 310 315 320
 Lys Ile Pro Leu Arg Asn Leu Val Gly Arg Ser Ile Glu Arg Pro Leu
 325 330 335
 Lys Ser Pro Leu Val Ser Lys Val Ile Thr Pro Pro Thr Pro Ile Ser
 340 345 350
 Val Gly Leu Ala Ala Ile Pro Val Thr His Ser Leu Ser Leu Ser Arg
 355 360 365
 Met Glu Ile Lys Glu Ile Ala Ser Arg Thr Arg Arg Glu Leu Leu Gly
 370 375 380
 Leu Ser Asp Glu Gly Gly Pro Lys Ser Glu Gly Ala Pro Lys Ala Lys
 385 390 395 400
 Ser Lys Pro Arg Lys Arg Leu Glu Glu Ser Gln Gly Gly Pro Lys Pro
 405 410 415
 Gly Ala Val Arg Ser Ser Ser Ser Asp Arg Ile Pro Ser Gly Ser Leu
 420 425 430
 Glu Ser Ala Ser Thr Ser Glu Ala Asn Pro Glu Gly His Ser Ala Ser
 435 440 445

Ser Asp Gln Asp Pro Val Ala Asp Arg Glu Gly Ser Pro Val Ser Gly
450 455 460

Ser Ser Pro Phe Gln Leu Thr Ala Phe Ser Asp Glu Asp Ile Ile Asp
465 470 475 480

Leu Lys

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GTTTAGTGAT ACGACACAAG ATCGGGAGAT TTTTGATCAC CATACTGAAG AGGATATAGA	60
TAAAAGTGCT AACAGTGTAT TGATAAAAAA CCTGAGCAGG ACCCCATCTA GTTGCAGCAG	120
CTCTCTGGAT TCAATCAAGG CTGATGGGAC CTCTCTGGAC TTCAGCACTT ACCGCAGTAG	180
TCAAATGGAA TCACAGTTTC TCAGAGATAC TATTTGTGAA GAGAGCTTGA GGGAGAAACT	240
CCAAGATGGG AGAATAACAA TAAGGGAGTT CTTTATACTT CTCCAGGTCC ACATCTTGAT	300
ACAGAAACCC CGACAGAGCA ATCTCCCAGG CAATTTTACT GTAAACACAC CACCTACTCC	360
AGAAGACCTG ATGTTAAGTC AATATGTTTA CCGACCCAAG ATACAGATTT ATAGAGAAGA	420
TTGTGAGGCT CGTCGCCAAA AGATTGAAGA ATTAAAGCTT TCTGCATCGA ACCAAGATAA	480
GCTGTTGGTT GATATAAATA AGAACCTGTG GGAAAAAATG AGACACTGCT CTGACAAAAGA	540
GCTGAAGGCC TTTGGAATTT ATCTTAACAA AATAAAGTCA TGTTTTACCA AGATGACTAA	600
AGTCTTCACT CACCAAGGAA AAGTGGCTCT GTATGGCAAG CTGGTGCAGT CAGCTCAGAA	660
TGAGAGGGAG AAACCTCAAA TAAAGATAGA TGAGATGGAT AAAATACTTA AGAAGATCGA	720
TAAGTGCTC ACTGAGATGG AAACAGAAAC TAAGAATTG GAGGATGAAG AGAAAAACAA	780
TCCTGTGGAA GAATGGGATT CTGAAATGAG AGCTGCAGAA AAAGAATTGG AACAGCTGAA	840
AACTGAAGAG GAGGAGCTTC AAAGAAATCT CTTAGAACTG GAGGTACCAA AAGAGCAGAC	900
CCTTGCTCAA ATAGACTTTA TGCAAAAACA AAGAAATAGA ACTGAAGAGC TACTGGATCA	960
GTTGAGCTTG TCTGAGTGGG ATGTCGTTGA GTGGAGTGAT GATCAAGCTG TATTCACCTT	1020
TGTTTATGAC ACGATACAAC TCACCATCAC CTTTGAAGAG TCAGTTGTTG GTTTCCTTTT	1080
CCTGGACAAG CGTTATAGGA AGATTGTTGA TGTCATTTT CAATCTCTGT TAGATGAGGA	1140
TCAAGCTCCT CCTTCCTCCC TTTTAGTTCA TAAGCTTATT TTCCAGTACG TTGAAGAAAA	1200
GGAATCCTGG AAGAAGACAT GTACAACCCA GCATCAGTTA CCCAAGATGC TTGAAGAATT	1260

CTCACTGGTA GTGCACCATT GCAGACTCCT TGGAGAGGAG ATTGAGTATT TAAAGAGATG 1320
 GGGACCAAAT TATAACCTAA TGAACATAGA TATTAATAAT AATGAATTGA GACTTTTATT 1380
 CTCTAGCTCC GCAGCATTTG CAAAGTTTGA AATAACTTTG TTTCTCTCAG CCTATTATCC 1440
 ATCTGTACCA TTACCTTCCA CCATTCAGAA TCACGTTGGG AACACTAGCC AAGATGATAT 1500
 TGCTACCATT CTATCTAAAG TGCCACTGGA GAACAACTAC CTGAAGAATG TAGTCAAGCA 1560
 AATTTACCAA GATCTGTTTC AGGACTGCCA TTTCTACCAC TAGACCCTTG GACCACCATT 1620
 GGAACAACCA AGCAGAATGT ACTTGATATT ATTCAGGGT CCCATTGCTG TTCAGCCTTT 1680
 GTTTTTACGT CATTACAAGC TGAGTAAAAT TCCTTCTGAT GATGTTATAA AAAAAAAAAA 1740
 AAAAAAAAAA 1748

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Glu	Ser	Gln	Phe	Leu	Arg	Asp	Thr	Ile	Cys	Glu	Glu	Ser	Leu	Arg	1	5	10	15
Glu	Lys	Leu	Gln	Asp	Gly	Arg	Ile	Thr	Ile	Arg	Glu	Phe	Phe	Ile	Leu	20	25	30	
Leu	Gln	Val	His	Ile	Leu	Ile	Gln	Lys	Pro	Arg	Gln	Ser	Asn	Leu	Pro	35	40	45	
Gly	Asn	Phe	Thr	Val	Asn	Thr	Pro	Pro	Thr	Pro	Glu	Asp	Leu	Met	Leu	50	55	60	
Ser	Gln	Tyr	Val	Tyr	Arg	Pro	Lys	Ile	Gln	Ile	Tyr	Arg	Glu	Asp	Cys	65	70	75	80
Glu	Ala	Arg	Arg	Gln	Lys	Ile	Glu	Glu	Leu	Lys	Leu	Ser	Ala	Ser	Asn	85	90	95	
Gln	Asp	Lys	Leu	Leu	Val	Asp	Ile	Asn	Lys	Asn	Leu	Trp	Glu	Lys	Met	100	105	110	
Arg	His	Cys	Ser	Asp	Lys	Glu	Leu	Lys	Ala	Phe	Gly	Ile	Tyr	Leu	Asn	115	120	125	
Lys	Ile	Lys	Ser	Cys	Phe	Thr	Lys	Met	Thr	Lys	Val	Phe	Thr	His	Gln	130	135	140	
Gly	Lys	Val	Ala	Leu	Tyr	Gly	Lys	Leu	Val	Gln	Ser	Ala	Gln	Asn	Glu	145	150	155	160

Arg Glu Lys Leu Gln Ile Lys Ile Asp Glu Met Asp Lys Ile Leu Lys
165 170 175

Lys Ile Asp Asn Cys Leu Thr Glu Met Glu Thr Glu Thr Lys Asn Leu
180 185 190

Glu Asp Glu Glu Lys Asn Asn Pro Val Glu Glu Trp Asp Ser Glu Met
195 200 205

Arg Ala Ala Glu Lys Glu Leu Glu Gln Leu Lys Thr Glu Glu Glu Glu
210 215 220

Leu Gln Arg Asn Leu Leu Glu Leu Glu Val Pro Lys Glu Gln Thr Leu
225 230 235 240

Ala Gln Ile Asp Phe Met Gln Lys Gln Arg Asn Arg Thr Glu Glu Leu
245 250 255

Leu Asp Gln Leu Ser Leu Ser Glu Trp Asp Val Val Glu Trp Ser Asp
260 265 270

Asp Gln Ala Val Phe Thr Phe Val Tyr Asp Thr Ile Gln Leu Thr Ile
275 280 285

Thr Phe Glu Glu Ser Val Val Gly Phe Pro Phe Leu Asp Lys Arg Tyr
290 295 300

Arg Lys Ile Val Asp Val Asn Phe Gln Ser Leu Leu Asp Glu Asp Gln
305 310 315 320

Ala Pro Pro Ser Ser Leu Leu Val His Lys Leu Ile Phe Gln Tyr Val
325 330 335

Glu Glu Lys Glu Ser Trp Lys Lys Thr Cys Thr Thr Gln His Gln Leu
340 345 350

Pro Lys Met Leu Glu Glu Phe Ser Leu Val Val His His Cys Arg Leu
355 360 365

Leu Gly Glu Glu Ile Glu Tyr Leu Lys Arg Trp Gly Pro Asn Tyr Asn
370 375 380

Leu Met Asn Ile Asp Ile Asn Asn Asn Glu Leu Arg Leu Leu Phe Ser
385 390 395 400

Ser Ser Ala Ala Phe Ala Lys Phe Glu Ile Thr Leu Phe Leu Ser Ala
405 410 415

Tyr Tyr Pro Ser Val Pro Leu Pro Ser Thr Ile Gln Asn His Val Gly
420 425 430

Asn Thr Ser Gln Asp Asp Ile Ala Thr Ile Leu Ser Lys Val Pro Leu
435 440 445

Glu Asn Asn Tyr Leu Lys Asn Val Val Lys Gln Ile Tyr Gln Asp Leu
450 455 460

Phe Gln Asp Cys His Phe Tyr His
465 470

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTTTCTTTG ATTGTCTCTG CTTTAGCGTC TCTAAATCCG GTCACCATGT CGGACCCCGA	60
AGGCGAGACC TTGCGAAGCA CCTTTCCTC TTATATGGCC GAAGGCGAGC GGCTCTACCT	120
GTGCGGGGAA TTTTCTAAAG CCGCGCAGAG CTTCAGCAAC GCTCTTTACC TTCAGGATGG	180
AGACAAGAAC TGCCTGGTTG CTCGCTCAAA GTGCTTCCTG AAGATGGGAG ACTTGAGAG	240
ATCCCTGAAG GATGCTGARG CTTGCTCCA GAGTGACCCA GCTTTCTGTA AGGGGATTTT	300
GCAAAGGCT GAGACACTGT ACACCATGGG AGACTTTGAG TTTGCCTTGG TATTCTATCA	360
TCGARGCTAC AAGCTGARGC CTGATCGGGA ATTCARARTT GGCATTCAGA AAGCCCAGGA	420
AGCCATCAAC AACTCAGTGG GAAGTCCTC TTCCATTAAG CTGGAGAACA AAGGGGACCT	480
CTCCTTCTTA AGCAAGCAGG CTGAGAATAT AAAAGCCCAG CAGAAGCCTC AGCCCATGAA	540
ACACCTCTTA CACCCACCA AGGGAGAGCC CAAGTGGAAG GCCTCGCTCA AGAGTGAGAA	600
GACTGTCCGC CAGCTTCTGG GGGAGCTCTA CGTGGACAAA GAGTATTTGG AGAAGCTCCT	660
ATTGGATGAA GACCTGATCA AAGGCACCAT GAAGGGCGGC CTGACTGTGG AGGACCTCAT	720
CATGACGGGC ATCAACTACC TGGATACTCA CAGCAACTTC TGGAGGCAGC AGAAGCCGAT	780
CTACGCCAGG GAGCGGGACC GGAAGCTGAT GCAAGAGAAA TGGCTGCGGG ACCACAAACG	840
CCGTCCCTCA CAGACAGCCC ATTACATCCT CAAGAGCCTG GAGGACATTG ATATGTTGCT	900
CACAAGTGGC AGTGCTGAAG GGAGTCTTCA GAAAGCTGAG AAAGTGCTGA AGAAGGTACT	960
GGAATGGAAC AAGGAAGAGG TACCCAACAA GGATGAACTG GTTGGAAGT TGTATAGCTG	1020
CATAGGGAAT GCCCAGATTG AGCTGGGGCA GATGGAGGCA GCCCTGCAGA GCCACAGAAA	1080
GGACYTGGAG ATCGCCAAGG AATATGACCT TCCTGATGCA AAATCGAGAG CCCTTGACAA	1140
CATTGGCAGA GTTTTTGCCA GAGTTGGGAA ATTCCAGCAA GCCATTGACA CGTGGGAAGA	1200
AAAGATCCCT CTGGCAAAAA CCACCCTGGA GAAGACCTGG CTGTTCCACG AGATCGGCCG	1260
CTGCTACTTG GAGCTGGACC AGGCCTGGCA GGCCAGAAT TATGGCGAGA AGTCCCAGCA	1320
GTGTGCCGAG GAGGAAGGGG ACATTGAGTG GCAACTGAAT GCCAGTGTTT TGGTGGCCCA	1380
GGCACAAGTG AAGCTGAGAG ACTTCGAGTC AGCCGTGAAC AATTTTGAGA AGGCCCTGGA	1440
GAGAGCAAAG CTTGTGCATA ACAACGAGGC GCAGCAGGCC ATCATCAGTG CCTTGACGA	1500

TGCCAACAAAG GGTATCATCA GAGAACTGAG GAAAACCAAC TACGTGGAGA ATCTCAAAGA	1560
AAAAAGCGAG GGAGAAGCTT CACTGTATGA AGATAGAATA ATAACAAGAG AGAAGGACAT	1620
GAGGAGAGTG AGAGATGAGC CCGAGAAGGT GGTGAAGCAG TGGGACCATA GTGAGGATGA	1680
GAAAGAGACA GATGAGGACG ATGAGGCTTT TGGGGAAGCT CTGCAGAGCC CAGCAAGCGG	1740
AAAGCAGAGT GTGGAAGCAG GAAAAGCCAG AAGCGATTG GGAGCAGTTG CCAAGGGCCT	1800
GTCAGGAGAA TTAGGCACAA GATCAGGAGA AACAGGCAGG AAGCTACTAG AAGCTGGCAG	1860
AAGAGAGTCA AGAGAAATTT ATAGGAGGCC TTCGGGAGAA TTAGAGCAAA GACTCTCAGG	1920
AGAATTCAGC AGACAGGAAC CAGAAGAACT AAAGAACTT TCAGAAGTGG GCAGAAGAGA	1980
SCCAGAAGAA YTGGGAAAAA CACAATTTGG AGAAATAGGA GAAACGAAAA AAACAGGAAA	2040
TGAGATGGAA AAGGAATATG AATGAAGCCA TCGGTAGAGA TGAGGATCAG GAAGCTGGTG	2100
TTCAGAGGGA TCATGGGATT TTATTAACT GGATTTTCAA GCGATTTGTC TGTTATAGGA	2160
AAAATGAGGG TTTTACTTYT GCTGCTTTCC ATCACTATTT TGCCATTAAA TAGGTGTCTT	2220
TCACTCTTGC MAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2280
AAAAAAAAAA AAAAAAAAAA	2298

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Ser	Asp	Pro	Glu	Gly	Glu	Thr	Leu	Arg	Ser	Thr	Phe	Pro	Ser	Tyr
1				5					10					15	
Met	Ala	Glu	Gly	Glu	Arg	Leu	Tyr	Leu	Cys	Gly	Glu	Phe	Ser	Lys	Ala
		20						25					30		
Ala	Gln	Ser	Phe	Ser	Asn	Ala	Leu	Tyr	Leu	Gln	Asp	Gly	Asp	Lys	Asn
	35						40					45			
Cys	Leu	Val	Ala	Arg	Ser	Lys	Cys	Phe	Leu	Lys	Met	Gly	Asp	Leu	Glu
	50					55					60				
Arg	Ser	Leu	Lys	Asp	Ala	Glu	Ala	Ser	Leu	Gln	Ser	Asp	Pro	Ala	Phe
65				70					75					80	
Cys	Lys	Gly	Ile	Leu	Gln	Lys	Ala	Glu	Thr	Leu	Tyr	Thr	Met	Gly	Asp
			85						90					95	
Phe	Glu	Phe	Ala	Leu	Val	Phe	Tyr	His	Arg	Xaa	Tyr	Lys	Leu	Xaa	Pro
			100					105					110		

Asp Arg Glu Phe Xaa Xaa Gly Ile Gln Lys Ala Gln Glu Ala Ile Asn
 115 120 125
 Asn Ser Val Gly Ser Pro Ser Ser Ile Lys Leu Glu Asn Lys Gly Asp
 130 135 140
 Leu Ser Phe Leu Ser Lys Gln Ala Glu Asn Ile Lys Ala Gln Gln Lys
 145 150 155 160
 Pro Gln Pro Met Lys His Leu Leu His Pro Thr Lys Gly Glu Pro Lys
 165 170 175
 Trp Lys Ala Ser Leu Lys Ser Glu Lys Thr Val Arg Gln Leu Leu Gly
 180 185 190
 Glu Leu Tyr Val Asp Lys Glu Tyr Leu Glu Lys Leu Leu Leu Asp Glu
 195 200 205
 Asp Leu Ile Lys Gly Thr Met Lys Gly Gly Leu Thr Val Glu Asp Leu
 210 215 220
 Ile Met Thr Gly Ile Asn Tyr Leu Asp Thr His Ser Asn Phe Trp Arg
 225 230 235 240
 Gln Gln Lys Pro Ile Tyr Ala Arg Glu Arg Asp Arg Lys Leu Met Gln
 245 250 255
 Glu Lys Trp Leu Arg Asp His Lys Arg Arg Pro Ser Gln Thr Ala His
 260 265 270
 Tyr Ile Leu Lys Ser Leu Glu Asp Ile Asp Met Leu Leu Thr Ser Gly
 275 280 285
 Ser Ala Glu Gly Ser Leu Gln Lys Ala Glu Lys Val Leu Lys Lys Val
 290 295 300
 Leu Glu Trp Asn Lys Glu Glu Val Pro Asn Lys Asp Glu Leu Val Gly
 305 310 315 320
 Asn Leu Tyr Ser Cys Ile Gly Asn Ala Gln Ile Glu Leu Gly Gln Met
 325 330 335
 Glu Ala Ala Leu Gln Ser His Arg Lys Asp Leu Glu Ile Ala Lys Glu
 340 345 350
 Tyr Asp Leu Pro Asp Ala Lys Ser Arg Ala Leu Asp Asn Ile Gly Arg
 355 360 365
 Val Phe Ala Arg Val Gly Lys Phe Gln Gln Ala Ile Asp Thr Trp Glu
 370 375 380
 Glu Lys Ile Pro Leu Ala Lys Thr Thr Leu Glu Lys Thr Trp Leu Phe
 385 390 395 400
 His Glu Ile Gly Arg Cys Tyr Leu Glu Leu Asp Gln Ala Trp Gln Ala
 405 410 415
 Gln Asn Tyr Gly Glu Lys Ser Gln Gln Cys Ala Glu Glu Glu Gly Asp
 420 425 430
 Ile Glu Trp Gln Leu Asn Ala Ser Val Leu Val Ala Gln Ala Gln Val

435	440	445
Lys Leu Arg Asp Phe Glu Ser Ala Val Asn Asn Phe Glu Lys Ala Leu 450 455 460		
Glu Arg Ala Lys Leu Val His Asn Asn Glu Ala Gln Gln Ala Ile Ile 465 470 475 480		
Ser Ala Leu Asp Asp Ala Asn Lys Gly Ile Ile Arg Glu Leu Arg Lys 485 490 495		
Thr Asn Tyr Val Glu Asn Leu Lys Glu Lys Ser Glu Gly Glu Ala Ser 500 505 510		
Leu Tyr Glu Asp Arg Ile Ile Thr Arg Glu Lys Asp Met Arg Arg Val 515 520 525		
Arg Asp Glu Pro Glu Lys Val Val Lys Gln Trp Asp His Ser Glu Asp 530 535 540		
Glu Lys Glu Thr Asp Glu Asp Asp Glu Ala Phe Gly Glu Ala Leu Gln 545 550 555 560		
Ser Pro Ala Ser Gly Lys Gln Ser Val Glu Ala Gly Lys Ala Arg Ser 565 570 575		
Asp Leu Gly Ala Val Ala Lys Gly Leu Ser Gly Glu Leu Gly Thr Arg 580 585 590		
Ser Gly Glu Thr Gly Arg Lys Leu Leu Glu Ala Gly Arg Arg Glu Ser 595 600 605		
Arg Glu Ile Tyr Arg Arg Pro Ser Gly Glu Leu Glu Gln Arg Leu Ser 610 615 620		
Gly Glu Phe Ser Arg Gln Glu Pro Glu Glu Leu Lys Lys Leu Ser Glu 625 630 635 640		
Val Gly Arg Arg Xaa Pro Glu Glu Leu Gly Lys Thr Gln Phe Gly Glu 645 650 655		
Ile Gly Glu Thr Lys Lys Thr Gly Asn Glu Met Glu Lys Glu Tyr Glu 660 665 670		

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGAAGAGCCA CCATCCCTGC CCCCCTTTTC CCACCGGGGA GTCTGTACAG AGATTTTCT	60
ACGTTTTTAT TTTTGCCTC AGAGGGATGG GATTGGGGAG GAGGGGATGG GCAGCGGAGG	120
GTTGGGGGCA TGGTCTGCAG GCTCATCTGT GTCCGCCTTT CACTCCACTA ATGCTGTCTC	180

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AGTGT TTTCT CTCTCTCTCT TTCGAGCTTG CACTCCGGTA CCCGACCCGG CGCCCTGGCC      240
CATCCCATGC CGGGGGGCCA GTGGAAAGAA GACAGGCCGT CCAGCCCGTG CCCGCCTGCG      300
GCGGGGGCAC CCAGCAAGCC CGCCCACCGC CCGCTGCCTC ACCTGCTTCG CCACAGACTC      360
TTGTTCCCAG CCCCTTGGGG CCTCCGTGTT TGGGGTGGGG GAGCTGCTTA GAGACTGTGC      420
CCGTCCTCGG CCCCCACCC TGAAGTGCCA GCACCACCAG CACCAGATCT TCCGCCGCCA      480
CACCGCATTG AGGACACGCC GGCCGGGCCG CTTCGTCTCA AGTTGTATAA AGTTGTCTCC      540
GTGTCCCCTC CTCCCTCTGC CCCCAGTGTT TCTTCTGATT TTTTTTCCC CTTTCCCTCC      600
CTCCCTCTCC GCATTCTTCC CTTGGTTCAG CACAGGTAAA ACGGTTCCCC TCCCTCCCTG      660
CCTTCATGGA TCACCAGCTC ACGTCATGTT GCCTTCTCTT TTCTTTGTGT GTGTGTTTAT      720
TTAAGTTATT TTTCTTCCTC CTCTCCCTTT TCTTTTGGC CCTCCCTCCC TCCCTCTTCT      780
GCCATGTAAC TGGAGGATGT GCTATGAGTT TGCAAACAGC TGGACTGTCA GGCTGCTTTT      840
TTTTCCAGAT GTTCTTCTTC TGCTTCCCTT TCCCCTCCTC TCCCCTCCTT TTCCTTCCTT      900
CCTTCCTTTC CTTGGAGCAC TGAGCACCAT TTGGAAGCTT GAGAGAAACC AAAATTAAAG      960
AGAGAAAGAG AGAGCGTGCA CGCTCCTGCT TTGTCAAAAA AAAAAAAAAA      1010

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(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Met Gly Ser Gly Gly Leu Gly Ala Trp Ser Ala Gly Ser Ser Val Ser
1           5           10           15
Ala Phe His Ser Thr Asn Ala Val Ser Val Phe Ser Leu Ser Leu Phe
20           25           30
Arg Ala Cys Thr Pro Val Pro Asp Pro Ala Pro Trp Pro Ile Pro Cys
35           40           45
Arg Gly Ala Ser Gly Lys Lys Thr Gly Arg Pro Ala Arg Ala Arg Leu
50           55           60
Arg Arg Gly His Pro Ala Ser Pro Pro Thr Ala Arg Cys Leu Thr Cys
65           70           75           80
Phe Ala Thr Asp Ser Cys Ser Gln Pro Leu Gly Ala Ser Val Phe Gly
85           90           95
Val Gly Glu Leu Leu Arg Asp Cys Ala Arg Pro Arg Pro Pro Thr Leu
100          105          110

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Lys Cys Gln His His Gln His Gln Ile Phe Arg Arg His Thr Ala Leu
115 120 125
Arg Thr Arg Arg Pro Gly Arg Phe Val Ser Ser Cys Ile Lys Leu Ser
130 135 140
Pro Cys Pro Leu Leu Pro Leu Pro Pro Val Phe Leu Leu Ile Phe Phe
145 150 155 160
Ser Pro Phe Pro Pro Ser Leu Ser Ala Phe Phe Pro Trp Phe Ser Thr
165 170 175
Gly Lys Thr Val Pro Leu Pro Pro Cys Leu His Gly Ser Pro Ala His
180 185 190
Val Met Leu Pro Ser Leu Phe Phe Val Cys Val Phe Ile
195 200 205

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTTYGCTCA TCAACCTCAT TATAGAACAT ATGATTTGTG ATACAGATCC TGAAGTTGGA 60
GGAGCAGTCC AGCTTATGGG CCTGCTTCGA ACTTTAGTTG ACCCAGAGAA CATGCTAGCC 120
ACTGCCMATA AAACASAAAA GACTGAATTT CTGGGTTTCT TCTACAAGCA CTGTATGCAT 180
GTTCTCWCTG CTCCTTTACT AGCAAATACA ACAGAAGACA AACCTAGTAA AGATGATTTT 240
CAGACTGCCC AACTATTGGC ACTTGTATTG GAATTGTTAA CATTTTGTGT GGAGCACCAT 300
ACCTACCACA TAAAGAACTA CATTATTAAT AAGGATATCC TCCGGAGAGT GCTAGTTCTT 360
ATGGCCTCGA AGCATGCTTT CTTGGCATTA TGTGCCCTTC GTTTTAAAAG AAAGATTATT 420
GGATTAAAAG ATGAGTTTTA CAACCGCTAC ATAATGAAAA GTTTTTTGTG TGAACCGATA 480
GTGAAAGCAT TTCTCAACAA TGGATCCCGC TACAATCTGA TGAAGTCTGC CATAATAGAG 540
ATGTTTGAAT TTATTAGAGT GGAAGATATA AAATCATTA CTGCTCATGT AATTGAAAAAT 600
TACTGGAAAG CACTGGAAGA TGTAAGATTAT GTACAGACAT TTAAAGGATT AAAACTGAGA 660
TTTGAACAAC AAAGAGAAAG GCAAGATAAT CCCAACTTG ACAGTATGCG TTCCATTTTG 720
AGGAATCACA GATATCGAAG AGATGCCAGA AACTAGAAG ATGAAGAAGA GATGTGGTTT 780
AACACAGATG AAGATGACAT GGAAGATGGA GAAGCTGTAG TGTCTCCATC TGACAAAAC 840
AAAAATGATG ATGATATTAT GGATCCAATA AGTAAATTCA TGGAAAGGAA GAAATTAAAA 900

GAAAGTGAGG AAAAGGAAGT GCTTCTGAAA ACAAACCTTT CTGGACGGCA GAGCCCAAGT	960
TTCAAGCTTT CCCTGTCCAG TGGAACGAAG ACTAACCTCA CCAGCCAGTC ATCTACAACA	1020
AATCTGCCTG GTTCTCCGGG ATCACCTGGA TCCCCAGGAT CTCCAGGCTC TCCTGGATCC	1080
GTACCTAAAA ATACATCTCA GACGGCAGCT ATTACTACAA AGGGAGGCCT CGTGGGTCTG	1140
GTAGATTATC CTGATGATGA TGAAGATGAT GATGAGGATG AAGATAAGGA AGATACGTTA	1200
CCATTGTCAA AGAAAGCAAA ATTTGATTCA TAATAATGGC AACGGCCTAG GATCAGTACC	1260
TGTTGAAAAA AACTGGTTCT CCACCCCTCC CCCATACAAA ATCCACAAAA AAGCGCAGTG	1320
GTCTCTTG TG AATGACTGAC ACAGATCAGC CTCTTACACT TGACTTCTGC TCATCAAGTG	1380
CCAATTCAAT GGAGCAGGAG GAGGGGATAT CATATATTTA GGGGAAAGAC TTAAGCCTTT	1440
GAGCTCTCCA GCTTGACCA CACATTGCCC TTTTCTCAGG GAAGGAAATG GAAACAAAAA	1500
GCCAACAGGG CAGGGGTTTT GTAAGTGGA CTCTGGATTG ACTGGTCAGT TGCTACAATC	1560
AGAATATGCT TTCTTGACC ATGTTTGAGA CTCAGAAGAA TGGCCTTTCT GCCATAATTC	1620
TTCCTAGTC AAGAATGCCA GCAGTTTCTT TGTATAAAGA GACCTGCCTT TAAAATCATA	1680
CATTCTGAAC ATTTTAGTCA AGCTACAACA GGTTTGAAA ACCTCTGTGG GGGAGGGGCG	1740
AGTATAAAGT TTTCTCTTT TTTAACTGTT CCCTTTGCCC TTCAAAGTGC AGATATTTTT	1800
TTTTTTAAGT GGGGACTTCT CCCTACTTGA TTAAAGATTG AGTGGAATTC TAGATGTGGT	1860
CATTTGTGTC ATAATTTTTT TGTTTTATTT TGTTTTTGAT TTTTTTTTTT CTCCCCTGAG	1920
TGTATGCTTA GTTGTTGAGT ATATATATTT GGGACCATTA AAACCTTTTTT TGATGTAATA	1980
TAACCTAACG TTGTGCTGGT ACCTGTTTTA CCATGTGTAA TTTTGTCTT ACATCACAGT	2040
TCTTAATTTG TTTAGAGTTT TATGAAAGAT GGTATAGTTT TTATTGACAA AAGCAAAGTA	2100
ATCTTACAAC TATGTGCATA CAAAAGCAAT ACTATTTTGT GACTAAATAT TTTATATTAA	2160
AATTTACATC AGCAACTGTC TTGAGAATTC AGGGAAATAG AATGGAATTT AAAACTTCAA	2220
CAGTTTTGTT AAATCTAGAA ACATGAAATT RGTATTCCAA AGAGATTCTG AAATTTCTTT	2280
TCTKGGGGAA ATGACGGTAC ATTAAATCAA AATTGRGGAT GGATGATTTA AAAACATTTG	2340
ACTTTTTAAT AATAAAAAGA AAAGTGAAGA GTAAGAGAAA TTGTAAAAAA AAAAAAAAAA	2400
AAAAAAAAA	2409

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Ile Cys Asp Thr Asp Pro Glu Leu Gly Gly Ala Val Gln Leu Met
1 5 10 15

Gly Leu Leu Arg Thr Leu Val Asp Pro Glu Asn Met Leu Ala Thr Ala
20 25 30

Xaa Lys Thr Xaa Lys Thr Glu Phe Leu Gly Phe Phe Tyr Lys His Cys
35 40 45

Met His Val Leu Xaa Ala Pro Leu Leu Ala Asn Thr Thr Glu Asp Lys
50 55 60

Pro Ser Lys Asp Asp Phe Gln Thr Ala Gln Leu Ala Leu Val Leu
65 70 75 80

Glu Leu Leu Thr Phe Cys Val Glu His His Thr Tyr His Ile Lys Asn
85 90 95

Tyr Ile Ile Asn Lys Asp Ile Leu Arg Arg Val Leu Val Leu Met Ala
100 105 110

Ser Lys His Ala Phe Leu Ala Leu Cys Ala Leu Arg Phe Lys Arg Lys
115 120 125

Ile Ile Gly Leu Lys Asp Glu Phe Tyr Asn Arg Tyr Ile Met Lys Ser
130 135 140

Phe Leu Phe Glu Pro Val Val Lys Ala Phe Leu Asn Asn Gly Ser Arg
145 150 155 160

Tyr Asn Leu Met Asn Ser Ala Ile Ile Glu Met Phe Glu Phe Ile Arg
165 170 175

Val Glu Asp Ile Lys Ser Leu Thr Ala His Val Ile Glu Asn Tyr Trp
180 185 190

Lys Ala Leu Glu Asp Val Asp Tyr Val Gln Thr Phe Lys Gly Leu Lys
195 200 205

Leu Arg Phe Glu Gln Gln Arg Glu Arg Gln Asp Asn Pro Lys Leu Asp
210 215 220

Ser Met Arg Ser Ile Leu Arg Asn His Arg Tyr Arg Arg Asp Ala Arg
225 230 235 240

Thr Leu Glu Asp Glu Glu Glu Met Trp Phe Asn Thr Asp Glu Asp Asp
245 250 255

Met Glu Asp Gly Glu Ala Val Val Ser Pro Ser Asp Lys Thr Lys Asn
260 265 270

Asp Asp Asp Ile Met Asp Pro Ile Ser Lys Phe Met Glu Arg Lys Lys
275 280 285

Leu Lys Glu Ser Glu Glu Lys Glu Val Leu Leu Lys Thr Asn Leu Ser
290 295 300

Gly Arg Gln Ser Pro Ser Phe Lys Leu Ser Leu Ser Ser Gly Thr Lys

305		310		315		320
Thr Asn Leu Thr	Ser Gln Ser Ser Thr Thr	Asn Leu Pro Gly Ser Pro				
	325	330				335
Gly Ser Pro Gly	Ser Pro Gly Ser Pro Gly Ser Pro Gly	Ser Val Pro				
	340	345				350
Lys Asn Thr Ser	Gln Thr Ala Ala Ile Thr Thr Lys Gly Gly Leu Val					
	355	360				365
Gly Leu Val Asp Tyr Pro Asp Asp Asp Glu Asp Asp Asp Glu Asp Glu						
	370	375				380
Asp Lys Glu Asp Thr Leu Pro Leu Ser Lys Lys Ala Lys Phe Asp Ser						
	385	390				395
						400

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 951 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCCAGGCAGG GTGTGGGGGC AGCTGTGCCA ATCTACCTCA CAGGCCACC CCCTGCCGGG	60
CATGCCGTGG GATCATGGGC AGGGAAGGCT CTGGGGGTCTG GAGACACCGC TGCTTAGCAC	120
CCCCAGCCAG AACACCCTGA GGGTCTCGGG GCTCTGGAGA GAGTGGGGCG GGAGGAAGAA	180
TTGGCACCTT CCTAGGGAAG GAGACGAGCG CTCGCCTTG ATTCTCCGAG AAGCCTCCGA	240
GAAGTGCTTT AAGTGTGTTT GCATGCSCCA GCGGGTGGGC AGCGGGGGCC TGTCCARCCC	300
TCTCCCGCCA TCCTTCCCCA AGTGACGTCC ACTGCCTTGT CACCAGCGAC CTGCCTGTCA	360
TGCCCCACCC CTGAGGAAGC ATGGGGACCC TAACACCCTG GTGCCCTGCA CCAGACAGGC	420
CGTGGTCAGG CCCAGGCCAC CGGCCGGGTT CTGCCACARC TTCCCACGTG CTTGCTGACA	480
TGCSTGTGCC TGTGTGTGGT GTCTGTTGCT GTGTCGTGAA ACTGTGACCA TCACTCAGTC	540
CAAACAAGTG AGTGGCCCTS GAGGCCACAG TTATGCAACT TTCAGTGTGT GTCATAACGA	600
CGTCACTGCT TTTTAAACTC GATAACTCTT TATTTTAGTA AAATGCCAG GAGTCCTGGA	660
AGCTACGCGG ACTTGAGAG GTTTTATTTT TTGGCCTTAG AATCTGCAGA AATTAGGAGG	720
CACCGAGCCC AGCGCAGCAG CCTCGGACCC GGATTGCGTT TGCCTTAGCG GATATGTTTA	780
TACAGATGAA TATAAATGT TTTTCTTTT GGGCTTTTCTTCTTTT CCCCCCTTC	840
TCACCTTCCC TTCTCCCTGA CCCCACCCCC CAAAAAGCT ACTTCTTCAT TCCGTGGTAC	900
GATTATTTTT TTTAACTAAA GGAAGATAAA ATTCTAAAAA AAAAAAAAAA A	951

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Pro Trp Asp His Gly Gln Gly Arg Leu Trp Gly Ser Glu Thr Pro
 1 5 10 15
 Leu Leu Ser Thr Pro Ser Gln Asn Thr Leu Arg Val Ser Gly Leu Trp
 20 25 30
 Arg Glu Trp Gly Gly Arg Lys Asn Trp His Leu Pro Arg Glu Gly Asp
 35 40 45
 Glu Arg Phe Ala Leu Ile Leu Arg Glu Ala Ser Glu Lys Cys Phe Lys
 50 55 60
 Cys Val Cys Met Xaa Gln Ala Val Gly Ser Gly Gly Leu Ser Xaa Pro
 65 70 75 80
 Leu Pro Pro Ser Phe Pro Lys
 85

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1899 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCCGCTTGT GTCCACGGGA CGCGGGCGGA TCTTCTCCGG CCATGAGGAA GCCAGCCGCT 60
 GGCTTCCTTC CCTCACTCCT GAAGGTGCTG CTCCTGCCTC TGGCACCTGC CGCAGCCCAG 120
 GATTCGACTC AGGCCTCCAC TCCAGGCAGC CCTCTCTCTC CTACCGAATA CGAACGCTTC 180
 TTCGCACTGC TGA CTCCAAC CTGGAAGGCA GAGACTACCT GCCGTCTCCG TGCAACCCAC 240
 GGCTGCCGGA ATCCCACACT CGTCCAGCTG GACCAATATG AAAACCACGG CTTAGTGCCC 300
 GATGGTGCTG TCTGCTCCAA CCTCCCTTAT GCCTCCTGGT TTGAGTCTTT CTGCCAGTTC 360
 ACTCACTACC GTTGCTCCAA CCACGTCTAC TATGCCAAGA GAGTCCTGTG TTCCCAGCCA 420
 GTCTCTATTC TCTCACCTAA CACTCTCAAG GAGATAGAAG CTTACAGCTGA AGTCTCACCC 480
 ACCACGATGA CCTCCCCCAT CTCACCCAC TTCACAGTGA CAGAACGCCA GACCTTCCAG 540
 CCCTGGCCTG AGAGGCTCAG CAACAACGTG GAAGAGCTCC TACAATCCTC CTTGTCCCTG 600

GGAGGCCAGG AGCAAGCGCC AGAGCACAAG CAGGAGCAAG GAGTGGAGCA CAGGCAGGAG	660
CCGACACAAG AACACAAGCA GGAAGAGGGG CAGAAACAGG AAGAGCAAGA AGAGGAACAG	720
GAAGAGGAGG GAAAGCAGGA AGAAGGACAG GGGACTAAGG AGGGACGGGA GGCTGTGTCT	780
CAGCTGCAGA CAGACTCAGA GCCCAAGTTT CACTCTGAAT CTCTATCTTC TAACCCTTCC	840
TCTTTTGCTC CCCGGGTACG AGAAGTAGAG TCTACTCCTA TGATAATGGA GAACATCCAG	900
GAGCTCATTC GATCAGCCCA GGAAATAGAT GAAATGAATG AAATATATGA TGAGAACTCC	960
TACTGGAGAA ACCAAAACCC TGGCAGCCTC CTGCAGCTGC CCCACACAGA GGCTTGCTG	1020
GTGCTGTGCT ATTCGATCGT GGAGAATACC TGCATCATAA CCCCCACAGC CAAGGCCTGG	1080
AAGTACATGG AGGAGGAGAT CCTTGGTTTC GGGAAAGTCGG TCTGTGACAG CCTTGGGCGG	1140
CGACACATGT CTACCTGTGC CCTCTGTGAC TTCTGCTCCT TGAAGCTGGA GCAGTGCCAC	1200
TCAGAGGCCA GCCTGCAGCG GCAACAATGC GACACCTCCC ACAAGACTCC CTTTGTGACG	1260
CCCTTGCTTG CCTCCCAGAG CCTGTCCATC GGCAACCAGG TAGGGTCCCC AGAATCAGGC	1320
CGCTTTTACG GGCTGGATTT GTACGGTGGG CTCCACATGG ACTTCTGGTG TGCCCGGCTT	1380
GCCACGAAAG GCTGTGAAGA TGTCCGAGTC TCTGGGTGGC TCCAGACTGA GTTCCTTAGC	1440
TTCCAGGATG GGGATTTCCC TACCAAGATT TGTGACACAG ACTATATCCA GTACCCAAAC	1500
TACTGTTCCT TCAAAAGCCA GCAGTGTCTG ATGAGAAACC GCAATCGGAA GGTGTCCCGC	1560
ATGAGATGTC TGCAGAAATGA GACTTACAGT GCGCTGAGCC TGGCAAAAGT GAGGACGTTG	1620
TGCTTTTCGAT GGAGCCAGGA GTTCAGCACC TTGACTCTAG GCCAGTTCGG ATGAGCTKGS	1680
GTTTATTTTG CCCACACCCC AGCCCAACCT GCCCASGTTT TCTATTGTTT TGAGACCCCA	1740
TTGCTTTCAG GCTGCCCCCTT CTGGGTCTGT TACTCGGCCC CTAMTCACAT TTCCTTGGGT	1800
TGGAGCAACA GTCCCAGAGA GGGCCACGGT GGGAGCTGCG CCCTCCTTAA AAGATGACTT	1860
TACATAAAAT GTTGATCTTC AAAAAAAAAA AAAAAAAAAA	1899

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Arg	Lys	Pro	Ala	Ala	Gly	Phe	Leu	Pro	Ser	Leu	Leu	Lys	Val	Leu
1				5					10					15	

Leu	Leu	Pro	Leu	Ala	Pro	Ala	Ala	Ala	Gln	Asp	Ser	Thr	Gln	Ala	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20										25					30				
Thr	Pro	Gly	Ser	Pro	Leu	Ser	Pro	Thr	Glu	Tyr	Glu	Arg	Phe	Phe	Ala				
		35					40					45							
Leu	Leu	Thr	Pro	Thr	Trp	Lys	Ala	Glu	Thr	Thr	Cys	Arg	Leu	Arg	Ala				
	50					55					60								
Thr	His	Gly	Cys	Arg	Asn	Pro	Thr	Leu	Val	Gln	Leu	Asp	Gln	Tyr	Glu				
65					70					75					80				
Asn	His	Gly	Leu	Val	Pro	Asp	Gly	Ala	Val	Cys	Ser	Asn	Leu	Pro	Tyr				
			85						90					95					
Ala	Ser	Trp	Phe	Glu	Ser	Phe	Cys	Gln	Phe	Thr	His	Tyr	Arg	Cys	Ser				
			100					105					110						
Asn	His	Val	Tyr	Tyr	Ala	Lys	Arg	Val	Leu	Cys	Ser	Gln	Pro	Val	Ser				
		115					120					125							
Ile	Leu	Ser	Pro	Asn	Thr	Leu	Lys	Glu	Ile	Glu	Ala	Ser	Ala	Glu	Val				
	130					135					140								
Ser	Pro	Thr	Thr	Met	Thr	Ser	Pro	Ile	Ser	Pro	His	Phe	Thr	Val	Thr				
145					150					155					160				
Glu	Arg	Gln	Thr	Phe	Gln	Pro	Trp	Pro	Glu	Arg	Leu	Ser	Asn	Asn	Val				
				165					170					175					
Glu	Glu	Leu	Leu	Gln	Ser	Ser	Leu	Ser	Leu	Gly	Gly	Gln	Glu	Gln	Ala				
			180					185					190						
Pro	Glu	His	Lys	Gln	Glu	Gln	Gly	Val	Glu	His	Arg	Gln	Glu	Pro	Thr				
		195					200					205							
Gln	Glu	His	Lys	Gln	Glu	Glu	Gly	Gln	Lys	Gln	Glu	Glu	Gln	Glu	Glu				
	210					215					220								
Glu	Gln	Glu	Glu	Glu	Gly	Lys	Gln	Glu	Glu	Gly	Gln	Gly	Thr	Lys	Glu				
225					230				235					240					
Gly	Arg	Glu	Ala	Val	Ser	Gln	Leu	Gln	Thr	Asp	Ser	Glu	Pro	Lys	Phe				
				245					250					255					
His	Ser	Glu	Ser	Leu	Ser	Ser	Asn	Pro	Ser	Ser	Phe	Ala	Pro	Arg	Val				
			260					265					270						
Arg	Glu	Val	Glu	Ser	Thr	Pro	Met	Ile	Met	Glu	Asn	Ile	Gln	Glu	Leu				
		275					280					285							
Ile	Arg	Ser	Ala	Gln	Glu	Ile	Asp	Glu	Met	Asn	Glu	Ile	Tyr	Asp	Glu				
	290					295					300								
Asn	Ser	Tyr	Trp	Arg	Asn	Gln	Asn	Pro	Gly	Ser	Leu	Leu	Gln	Leu	Pro				
305					310					315				320					
His	Thr	Glu	Ala	Leu	Val	Leu	Cys	Tyr	Ser	Ile	Val	Glu	Asn	Thr					
			325					330					335						
Cys	Ile	Ile	Thr	Pro	Thr	Ala	Lys	Ala	Trp	Lys	Tyr	Met	Glu	Glu	Glu				
			340					345					350						

Ile Leu Gly Phe Gly Lys Ser Val Cys Asp Ser Leu Gly Arg Arg His
355 360 365

Met Ser Thr Cys Ala Leu Cys Asp Phe Cys Ser Leu Lys Leu Glu Gln
370 375 380

Cys His Ser Glu Ala Ser Leu Gln Arg Gln Gln Cys Asp Thr Ser His
385 390 395 400

Lys Thr Pro Phe Val Ser Pro Leu Leu Ala Ser Gln Ser Leu Ser Ile
405 410 415

Gly Asn Gln Val Gly Ser Pro Glu Ser Gly Arg Phe Tyr Gly Leu Asp
420 425 430

Leu Tyr Gly Gly Leu His Met Asp Phe Trp Cys Ala Arg Leu Ala Thr
435 440 445

Lys Gly Cys Glu Asp Val Arg Val Ser Gly Trp Leu Gln Thr Glu Phe
450 455 460

Leu Ser Phe Gln Asp Gly Asp Phe Pro Thr Lys Ile Cys Asp Thr Asp
465 470 475 480

Tyr Ile Gln Tyr Pro Asn Tyr Cys Ser Phe Lys Ser Gln Gln Cys Leu
485 490 495

Met Arg Asn Arg Asn Arg Lys Val Ser Arg Met Arg Cys Leu Gln Asn
500 505 510

Glu Thr Tyr Ser Ala Leu Ser Leu Ala Lys Val Arg Thr Leu Cys Phe
515 520 525

Arg Trp Ser Gln Glu Phe Ser Thr Leu Thr Leu Gly Gln Phe Gly
530 535 540

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 722 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGACCTTCCC AGCAATATGC ATCTTGCACG TCTGGTCGGC TCCTGCTCCC TCCTTCTGCT	60
ACTGGGGGCC CTGTCTGGAT GGGCGGCCAG CGATGACCCC ATTGAGAAGG TCATTGAAGG	120
GATCAACCGA GGGCTGAGCA ATGCAGAGAG AGAGGTGGGC AAGGCCCTGG ATGGCATCAA	180
CAGTGAATC ACGCATGCCG GAAGGGAAGT GGAGAAGGTT TTCAACGGAC TTAGCAACAT	240
GGGGAGCCAC ACCGGCAAGG AGTTGGACAA AGGCGTCCAG GGGCTCAACC ACGGCATGGA	300
CAAGGTTGCC CATGAGATCA ACCATGGTAT TGGACAAGCA GGAAAGGAAG CAGAGAAGCT	360

TGGCCATGGG GTCAACAACG CTGCTGGACA GGGCAACCAT CAAAGCGGAT CTTCCAGCCA	420
TCAAGGAGGG GCCACAACCA CGCCGTTAGC CTCTGGGGCC TCGGTCAACA CGCCTTTCAT	480
CAACCTTCCC GCCCTGTGGA GGAGCGTCGC CAACATCATG CCCTAAACTG GCATCCGGCC	540
TTGCTGGGAG AATAATGTCG CCGTTGTCAC ATCAGCTGAC ATGACCTGGA GGGGTTGGGG	600
GTGGGGGACA GGTTTCTGAA ATCCCTGAAG GGGGTTGTAC TGGGATTTGT GAATAAACTT	660
GATACACTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	720
AA	722

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	Leu	
1				5					10					15		
Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	Lys	Val	
			20					25					30			
Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	Glu	Val	Gly	
		35					40					45				
Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	Ala	Gly	Arg	Glu	
	50					55					60					
Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	Gly	Ser	His	Thr	Gly	
65					70					75					80	
Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	Asn	His	Gly	Met	Asp	Lys	
				85					90					95		
Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	Gly	Gln	Ala	Gly	Lys	Glu	Ala	
			100					105					110			
Glu	Lys	Leu	Gly	His	Gly	Val	Asn	Asn	Ala	Ala	Gly	Gln	Gly	Asn	His	
		115					120					125				
Gln	Ser	Gly	Ser	Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	
	130					135					140					
Ala	Ser	Gly	Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	
145					150				155						160	
Trp	Arg	Ser	Val	Ala	Asn	Ile	Met	Pro								
					165											

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AATGGCTTTT CTTCCTTCCT GGGTTTGTGT ACTAGTTGGT TCCTTTTCTG CTTCCTTAGC	60
AGGGACTTCC AATCTCTCAG AGACAGAGCC CCCTCTGTGG AAGGAGAGTC CTGGTCAGCT	120
CAGTGACTAC AGGGTGGAGA ACAGCATGTA CATTATTAAT CCCTGGGTAT ACCTTGAGAG	180
AATGGGGATG TATAAAATCA TATTGAATCA GACAGCCAGG TATTTTGCAA AATTTGCACC	240
AGATAATGAA CAGAATATTT TATGGGGGTT GCCTCTGCAG TATGGCTGGC AATATAGGAC	300
AGGCAGATTA GCTGATCCAA CCCGAAGGAC AACTGTGGC TATGAATCTG GAGATCATAT	360
GTGCATCTCT GTGGACAGTT GGTGGGCTGA TTTGAATTAT TTTCTGTCTT CATTACCCTT	420
TCTTGCTGCG GTTGATTCTG GTGTAATGGG GATATCATCA GACCAAGTCA GGCTTTTGCC	480
CCCACCCAAG AATGAGAGGA AGTTTGTGA TGATGTTTCT AGCTGTCGTT CATCCTTCCC	540
TGAGACAATG AACAAGTGGA ACACCTTTTA CCAGTATTTG CAGTCACCTT TTAGTAAGTT	600
TGATGATCTG TTGAAGTACT TATGGGCTGC ACACACTTCA ACCTTGGCAG ATAATATCAA	660
AAGTTTTGAA GACAGATATG ATTATTATTC TAAAGCAGAA GCGCATTTTG AGAGAAGTTG	720
GGTACTGGCT GTGGATCATT TAGCTGCAGT CCTCTTTCCT ACAACCTTGA TTAGATCATA	780
TAAGTTCCAG AAGGGCATGC CACCACGAAT TCTTCTTAAT ACTGATGTAG CCCCTTTCAT	840
CAGTGACTTT ACTGCTTTTC AGAATGTAGT CCTGGTTCTT CTAAATATGC TTGACAATGT	900
GGATAAATCT ATAGGTTATC TTTGTACAGA AAAATCTAAT GTATATAGAG ATCATTCGGA	960
ATCTAGCTCT AGAAGTTATG GAAATAACTC CTGAAACATT TAACTTCAAA CTTCAGGAAA	1020
TGATTAATGA ATTAAAAATG AAAAAGCTCGA ACTTGACAAT CAGTAATTTT AAAAAATTAA	1080
TGTCATCATG ACCATGTAGT TTATTCTTTC TGATATTTTT GATTTATGCT TATTTGTTAA	1140
GATCTTGATC ATGTATTAAA AACTTAAATT AAATGCATTC AAGTTAAAAA AAAAAAAAAA	1200
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1240

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met	Ala	Phe	Leu	Pro	Ser	Trp	Val	Cys	Val	Leu	Val	Gly	Ser	Phe	Ser	1	5	10	15
Ala	Ser	Leu	Ala	Gly	Thr	Ser	Asn	Leu	Ser	Glu	Thr	Glu	Pro	Pro	Leu	20	25	30	
Trp	Lys	Glu	Ser	Pro	Gly	Gln	Leu	Ser	Asp	Tyr	Arg	Val	Glu	Asn	Ser	35	40	45	
Met	Tyr	Ile	Ile	Asn	Pro	Trp	Val	Tyr	Leu	Glu	Arg	Met	Gly	Met	Tyr	50	55	60	
Lys	Ile	Ile	Leu	Asn	Gln	Thr	Ala	Arg	Tyr	Phe	Ala	Lys	Phe	Ala	Pro	65	70	75	80
Asp	Asn	Glu	Gln	Asn	Ile	Leu	Trp	Gly	Leu	Pro	Leu	Gln	Tyr	Gly	Trp	85	90	95	
Gln	Tyr	Arg	Thr	Gly	Arg	Leu	Ala	Asp	Pro	Thr	Arg	Arg	Thr	Asn	Cys	100	105	110	
Gly	Tyr	Glu	Ser	Gly	Asp	His	Met	Cys	Ile	Ser	Val	Asp	Ser	Trp	Trp	115	120	125	
Ala	Asp	Leu	Asn	Tyr	Phe	Leu	Ser	Ser	Leu	Pro	Phe	Leu	Ala	Ala	Val	130	135	140	
Asp	Ser	Gly	Val	Met	Gly	Ile	Ser	Ser	Asp	Gln	Val	Arg	Leu	Leu	Pro	145	150	155	160
Pro	Pro	Lys	Asn	Glu	Arg	Lys	Phe	Cys	Tyr	Asp	Val	Ser	Ser	Cys	Arg	165	170	175	
Ser	Ser	Phe	Pro	Glu	Thr	Met	Asn	Lys	Trp	Asn	Thr	Phe	Tyr	Gln	Tyr	180	185	190	
Leu	Gln	Ser	Pro	Phe	Ser	Lys	Phe	Asp	Asp	Leu	Leu	Lys	Tyr	Leu	Trp	195	200	205	
Ala	Ala	His	Thr	Ser	Thr	Leu	Ala	Asp	Asn	Ile	Lys	Ser	Phe	Glu	Asp	210	215	220	
Arg	Tyr	Asp	Tyr	Tyr	Ser	Lys	Ala	Glu	Ala	His	Phe	Glu	Arg	Ser	Trp	225	230	235	240
Val	Leu	Ala	Val	Asp	His	Leu	Ala	Ala	Val	Leu	Phe	Pro	Thr	Thr	Leu	245	250	255	
Ile	Arg	Ser	Tyr	Lys	Phe	Gln	Lys	Gly	Met	Pro	Pro	Arg	Ile	Leu	Leu	260	265	270	
Asn	Thr	Asp	Val	Ala	Pro	Phe	Ile	Ser	Asp	Phe	Thr	Ala	Phe	Gln	Asn	275	280	285	
Val	Val	Leu	Val	Leu	Leu	Asn	Met	Leu	Asp	Asn	Val	Asp	Lys	Ser	Ile	290	295	300	
Gly	Tyr	Leu	Cys	Thr	Glu	Lys	Ser	Asn	Val	Tyr	Arg	Asp	His	Ser	Glu				

305

310

315

320

Ser Ser Ser Arg Ser Tyr Gly Asn Asn Ser
325 330

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GCAGCACCAG	CCGTCTGCAG	CTCCGGCCGC	CACTTGCGCC	TCTCCAGCCT	CCGCAGGCCC	60
AACCGCCGCC	AGCACCATGG	CCAGCACCAT	TTCCGCCTAC	AAGGAGAAGA	TGAAGGAGCT	120
GTCGGTGCTG	TCGCTCATCT	GCTCCTGCTT	CTACACACAG	CCGCACCCCA	ATACCGTCTA	180
CCAGTACGGG	GACATGGAGG	TGAAGCAGCT	GGACAAGCGG	GCCTCAGGCC	AGAGCTTCGA	240
GGTCATCCTC	AAGTCCCCTT	CTGACCTGTC	CCCAGAGAGC	CCTATGCTCT	CCTCCCCACC	300
CAAGAAGAAG	GACACCTCCC	TGGAGGAGCT	GCAAAAGCGG	CTGGAGGCAG	CCGAGGAGCG	360
GAGGAAGACG	CAGGAGGCGC	AGGTGCTGAA	GCAGCTGGCG	GAGCGGCGCG	AGCACGAGCG	420
CGAGGTGCTG	CACAAGGCGC	TGGAGGAGAA	TAACAACCTT	AGCCGCCAGG	CGGAGGAGAA	480
GCTCAACTAC	AAGATGGAGC	TCAGCAAGGA	GATCCGCGAG	GCACACCTGG	CCGCACTGCG	540
CGAGCGGCTG	CGCGAGAAGG	AGCTGCACGC	GGCCGAGGTG	CGCAGGAACA	AGGAGCAGCG	600
AGAAGAGATG	TCGGGCTAAG	GGCCCgggac	GGGCGGCGCC	CATCCTGCGA	CAGAACACGT	660
TCGGGTTTTG	GTTTTGTTTC	GTTACCTCT	GTCTAGATGC	AACTTTTGTT	CCTCCTCCCC	720
CACCCCAGCC	CCCAGCTTCA	TGCTTCTCTT	CCGCACTCAG	CCGCCCTGCC	CTGTCCTCGT	780
GGTGAGTCGC	TGACCACGGC	TTCCCCTGCA	GGAGCCGCCG	GGCGTGAGAC	GCGGTCCCCTC	840
GGTGACAGACA	CCAGGCCGGG	CGCGGCTGGG	TCCCCCGGGG	GCCCTGTGAG	AGAGGTGGCG	900
GTGACCGTGG	TAAACCCAGG	GCGGTGGCGT	GGGATCGCGG	GTCCTTACGC	TGGGCTGTCT	960
GGTCAGCACG	TGCAGGTCAG	GGCAGGTCCT	CTGAGCCGGC	GCCCCCTGGC	AGCAGGCGAG	1020
GCTACAGTAC	CTGCTGTCTT	TCCAGGGGGA	AGGGGCTCCC	CATGAGGGAG	GGGCGACGGG	1080
GGAGGGGGGT	GATGGTGCCT	GGGAGCCTGC	GTGTGCAGCC	GGTGCTTGTT	GAACTGGCAG	1140
GCGGGTGGGT	GGGGGCTGCA	GCTTTCCTTA	ATGTGGTTGC	ACAGGGGTCC	TCTGAGACCA	1200
CCTGGCGTGA	GGTGGACACC	CTGGGCCTTC	CTGGAAGCCT	GCAGTTGGGG	GCCTGCCCTG	1260
AGTCTGCTGG	GGAGTGGGCA	TTCTCTGCCA	GGGACCCATG	AGCAGGCTGC	ATGGTCTAGA	1320

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GGTTGTGGGC AGCATGGACA GTCCCCCACT CAGAAGTGCA AGAGTTCCAA AGAGCCTCTG      1380
GCCCAGGCCC CTCCCCACCA GGGCTTTGCA GATGTCCTTG AAAGACCCAC CCTAGAGCCC      1440
TTTGGAGTGC TGGCCCCCTCC TGTGCCCTCT GCCCTGGTGG AAGCGGCAGC CACAAGTCCT      1500
CCTCAGGGAG CCCCAAGGGG GATTTTGTGG GACCGCTGCC CACAGATCCA GGTGTTGGAA      1560
GGGCAGCGGG TAAGGTTCCC AAGCCAGCCC CAACACCCTT CCCACTTGGC ACCCAGAGGG      1620
GGCTGTGGGT GGAGGCCTGA CTCCAGGCCT CTCCTGCCCA CACCCTCTGG GCTGAGTTCC      1680
TTCTTTCCCT TGGACGCCCA GTGCTGGCCT TGGAGGACGG TCAGCTGGAG GATGGCGGTG      1740
GGGGAGGCTG TCTTTGTACC ACTGCAGCAT CCCCCACTTC TCCACGGAAG CCCCATCCCA      1800
AAGCTGCTGC CTGGCCCCTT GCTGTAAAGT GTGAAGGGGG CGGCTGAGTT CTCTTAGGAC      1860
CCAGAGCCAG GGCCCTCAAC TTCCATCCTG CGGGAGGCCT TGGCCGGGCA CTGCCAGTGT      1920
CTTCCAGAGC CACACCCAGG GACCACGGGA GGATCCTGAC CCCTGCAGGG CTCAGGGGTC      1980
AGCAGGGACC CACTGCCCCA TCTCCCTCTC CCCACCAAGA CAGCCCCAGA AGGAGCAGCC      2040
AGCTGGGATG GGAACCCAAG GCTGTCCACA TCTGGCTTTT GTGGGACTCA GAAAGGGAAG      2100
CAGAACTGAG GGCTGGGATA TTCCTCATGG TGGCAGCGCT CATAGCGAAA GCCTACTGTA      2160
ATATGCACCC ATCTCATCCA CGTAGTAAAG TGAAC TAAA AATTCAATCA AATGAACAAT      2220
TAAATAAACA CCTGTGTGTT TAAGAAAAAA AAAAAAAAAA A                        2261

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(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

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Met Ala Ser Thr Ile Ser Ala Tyr Lys Glu Lys Met Lys Glu Leu Ser
1           5           10           15
Val Leu Ser Leu Ile Cys Ser Cys Phe Tyr Thr Gln Pro His Pro Asn
20          25          30
Thr Val Tyr Gln Tyr Gly Asp Met Glu Val Lys Gln Leu Asp Lys Arg
35          40          45
Ala Ser Gly Gln Ser Phe Glu Val Ile Leu Lys Ser Pro Ser Asp Leu
50          55          60
Ser Pro Glu Ser Pro Met Leu Ser Ser Pro Pro Lys Lys Lys Asp Thr
65          70          75          80
Ser Leu Glu Glu Leu Gln Lys Arg Leu Glu Ala Ala Glu Glu Arg Arg
85          90          95

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Lys Thr Gln Glu Ala Gln Val Leu Lys Gln Leu Ala Glu Arg Arg Glu
100 105 110
His Glu Arg Glu Val Leu His Lys Ala Leu Glu Glu Asn Asn Asn Phe
115 120 125
Ser Arg Gln Ala Glu Glu Lys Leu Asn Tyr Lys Met Glu Leu Ser Lys
130 135 140
Glu Ile Arg Glu Ala His Leu Ala Ala Leu Arg Glu Arg Leu Arg Glu
145 150 155 160
Lys Glu Leu His Ala Ala Glu Val Arg Arg Asn Lys Glu Gln Arg Glu
165 170 175
Glu Met Ser Gly
180

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGCCAAAGAG GCCTAGGAGC CTCGTGGCTG CGTCACCGCC GCCCCCCCAG ACAAGATGGA	60
CACCGCGGAG GAAGACATAT GTAGAGTGTG TCGGTCAGAA GGAACACCTG AGAAACCGCT	120
TTATCATCCT TGTGTATGTA CTGGCAGTAT TAAGTTTATC CATCAAGAAT GCTTAGTTCA	180
ATGGCTGAAA CACAGTCGAA AAGAATACTG TGAATTATGC AAGCACAGAT TTGCTTTTAC	240
ACCAATTTAT TCTCCAGATA TGCCTTCACG GCTTCCAATT CAAGACATAT TTGCTGGACT	300
GGTTACAAGT ATTGGCACTG CAATACGATA TTGGTTTCAT TATACACTTG TGGCCTTTGC	360
ATGGTTGGGA GTTGTTCCTC TTACAGCATG CCGCATCTAC AAGTGCTTGT TTAGTGGCTC	420
CCGTGAGCTC ACTACTGACG CTGCCCATTA GATATGCTGT CAACCGGAAA ATTTGTTGGC	480
AGATTGTTTG CAGGGTTGTT TTGTGGTGAC GTGCACACTG TGTGCATTCA TCAGCCTGGT	540
GTGGTTGAGA GAGCAGATAG TCCATGGGGG AGCACCAATT TGGTTGGAGC ATGCTGCCCC	600
ACCGTTCAAT GCTGCGGGG ATCACCAAAA TGAGGCTCCA GCAGGAGGAA ATGGTGCAGA	660
AAATGTTGCT GCTGATCAGC CTGCTAACCC ACCAGCTGAG AACGCAGTGG TGGGGGAAAA	720
CCCTGATGCC CAGGATGACC AGGCAGAAGA GGAGGAGGAG GACAATGAGG AGGAAGATGA	780
CGCTGGTGTG GAGGATGGCG GCAGATGCTA ATAACGGAGC CCAGGATGAC ATGAATTGGA	840
ATGCTTTAGA ATGGGACCGA GCTGCTGAAG AGCTTACATG GGAAAGAATG CTAGGACTTG	900

ATGGATCACT AGTTTTTCTG GAACATGTCT TCTGGGTGGT ATCTTTAAAT ACACTGTTCA	960
TTCTTGTTTT TGCATTTTGC CCTTACCATA TTGGTCATTT CTCCCTTGTT GGTGGGAT	1020
TTGAAGAACA CGTCCAAGCA TCTCATTTTG AAGGCCTAAT CACAACCATA GTTGGGTATA	1080
TACTTTTAGC AATAAACTG ATAATTTGTC ATGGCTTGGC AACTCTTG TG AAATTTTATA	1140
GATCTCGTCG CTTACTGGGA GTCTGCTATA TTGTTGTTAA GGTCTCTTTG TTAGTGGTGG	1200
TAGAAATTGG AGTATTCCT CTCATTTGTG GTTGGTGGCT GGATATCTGT TCCTTGAAA	1260
TGTTTGATGC TACTCTGAAA GATCGAGAAC TGAGCTTTCA GTCGGCTCCA GGTACTACCA	1320
TGTTTCTGCA TTGGCTAGTG GGAATGGTAT ATGTCTTCTA CTTTGCCTCC TTCATTCTAT	1380
TACTGAGAGA GGTACTTCGA CCTGGTGTCC TGTGGTTTCT AAGGAATTTG AATGATCCAG	1440
ATTTCAATCC AGTACAGGAA ATGATCCATT TGCCAATATA TAGGCATCTC CGAAGATTTA	1500
TTTTGTCACT GATTGTCTTT GGCTCCATTG TCCTCTGAT GCTTTGGCTT CCTATACGTA	1560
TAATTAAGAG TGTGCTGCCT AATTTTCTTC CATAAATGT CATGCTCTAC AGTGATGCTC	1620
CAGTGAGTGA ACTGTCCCTC GAGCTGCTTC TGCTTCAGGT TGTCTTGCCA GCATTACTCG	1680
AACAGGGACA CACGAGGCAG TGGCTGAAGG GGCTGGTGCG AGCGTGGACT GTGACCGCCG	1740
GATACTTGCT GGATCTTCAT TCTTATTTAT TGGGAGACCA GGAAGAAAAT GAAAACAGTG	1800
CAAATCAACA AGTTAACAAT AATCAGCATG CTCGAAATAA CAACGCTATT CCTGTGGTGG	1860
GAGAAGGCCT TCATGCAGCC CACCAAGCCA TACTCCAGCA GGGAGGGCCT GTTGGCTTTC	1920
AGCCTTACCG CCGACCTTTA AATTTTCCAC TCAGGATATT TCTGTTGATT GTCTTCATGT	1980
GTATAACATT ACTGATTGCC AGCCTCATCT GCCTTACTTT ACCAGTATTT GCTGGCCGTT	2040
GGTTAATGTC GTTTTGGACG GGGACTGCCA AAATCCATGA GCTCTACACA GCTGCTTG TG	2100
GTCTCTATGT TTGCTGGCTA ACCATAAGGG CTGTGACGGT GATGGTGGCA TGGATGCCTC	2160
AGGGACGCAG AGTGATCTTC CAGAAGGTTA AAGAGTGGTCT TCTCATGATC ATGAAGACTT	2220
TGATAGTTGC GGTGCTGTTG GCTGGAGTTG TCCCTCTCCT TCTGGGGCTC CTGTTTGAGC	2280
TGGTCATTGT GGCTCCCCTG AGGGTTCCCT TGGATCAGAC TCCTCTTTT TATCCATGGC	2340
AGGACTGGGC ACTTGGAGTC CTGCATGCCA AAATCATTGC AGCTATAACA TTGATGGGTC	2400
CTCAGTGGTG GTTGAAAAC GTAATTGAAC AGGTTTACGC AAATGGCATC CGGAACATTG	2460
ACCTTCACTA TATTGTTTCTG AACTGGCAG CTCCCGTGAT CTCTGTGCTG TTGCTTTCCC	2520
TGTGTGTACC TTATGTCATA GCTTCTGGTG TTGTTCTTT ACTAGGTGTT ACTGCGGAAA	2580
TGCAAAACTT AGTCCATCGG CGGATTTATC CATTTTACT GATGGTCGTG GTATTGATGG	2640
CAATTTTGTG CTTCCAAGTC CGCCAGTTTA AGCGCCTTTA TGAACATATT AAAAATGACA	2700
AGTACCTTGK GGGTCAASGA CTCGGTGAAC TACGAACGGA AATCTGGGCA AACAAGGCTC	2760

ATCTCCACCA CCTCCACAGT CATCCCAAGA ATAAAGTAGT TGTCTCAACA ACTTGACCTT 2820
 CCCCTTTACA TGTCTTTTTT TGTGGACTTC TCTCTTKGGA GATTTTTCCC AGTGATCTCT 2880
 CAGCGTKGTT TTTAAGTTAA AKGTATTKGA CTTGTGTTCT CAGCATTCAG AGAGCAGCGG 2940
 TGTAAGATTC TGCTGTTCTC CCTGGATCTT CTGACATKAC TGCTGTCTGA GATTTGTATA 3000
 TGKGTAAATA CAAGTTCCTT GATACCCTAA AACCTTGGAT TAAACAGAAT GTGCATKGTA 3060
 CATCTTTAAA CAAATGKAT ATTAATTTAT TAAAAA AAAA 3109

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Gly	Glu	His	Gln	Phe	Gly	Trp	Ser	Met	Leu	Pro	His	Arg	Ser	Met	1	5	10	15
Leu	Arg	Gly	Ile	Thr	Lys	Met	Arg	Leu	Gln	Gln	Glu	Glu	Met	Val	Gln	20	25	30	
Lys	Met	Leu	Leu	Ile	Ser	Leu	Leu	Thr	His	Gln	Leu	Arg	Thr	Gln	35	40	45		
Trp	Trp	Gly	Lys	Thr	Leu	Met	Pro	Arg	Met	Thr	Arg	Gln	Lys	Arg	Arg	50	55	60	
Arg	Arg	Thr	Met	Arg	Arg	Lys	Met	Thr	Leu	Val	Trp	Arg	Met	Ala	Ala	65	70	75	80
Asp	Ala	Asn	Asn	Gly	Ala	Gln	Asp	Asp	Met	Asn	Trp	Asn	Ala	Leu	Glu	85	90	95	
Trp	Asp	Arg	Ala	Ala	Glu	Glu	Leu	Thr	Trp	Glu	Arg	Met	Leu	Gly	Leu	100	105	110	
Asp	Gly	Ser	Leu	Val	Phe	Leu	Glu	His	Val	Phe	Trp	Val	Val	Ser	Leu	115	120	125	
Asn	Thr	Leu	Phe	Ile	Leu	Val	Phe	Ala	Phe	Cys	Pro	Tyr	His	Ile	Gly	130	135	140	
His	Phe	Ser	Leu	Val	Gly	Leu	Gly	Phe	Glu	Glu	His	Val	Gln	Ala	Ser	145	150	155	160
His	Phe	Glu	Gly	Leu	Ile	Thr	Thr	Ile	Val	Gly	Tyr	Ile	Leu	Leu	Ala	165	170	175	
Ile	Thr	Leu	Ile	Ile	Cys	His	Gly	Leu	Ala	Thr	Leu	Val	Lys	Phe	His	180	185	190	

Arg Ser Arg Arg Leu Leu Gly Val Cys Tyr Ile Val Val Lys Val Ser
195 200 205

Leu Leu Val Val Val Glu Ile Gly Val Phe Pro Leu Ile Cys Gly Trp
210 215 220

Trp Leu Asp Ile Cys Ser Leu Glu Met Phe Asp Ala Thr Leu Lys Asp
225 230 235 240

Arg Glu Leu Ser Phe Gln Ser Ala Pro Gly Thr Thr Met Phe Leu His
245 250 255

Trp Leu Val Gly Met Val Tyr Val Phe Tyr Phe Ala Ser Phe Ile Leu
260 265 270

Leu Leu Arg Glu Val Leu Arg Pro Gly Val Leu Trp Phe Leu Arg Asn
275 280 285

Leu Asn Asp Pro Asp Phe Asn Pro Val Gln Glu Met Ile His Leu Pro
290 295 300

Ile Tyr Arg His Leu Arg Arg Phe Ile Leu Ser Val Ile Val Phe Gly
305 310 315 320

Ser Ile Val Leu Leu Met Leu Trp Leu Pro Ile Arg Ile Ile Lys Ser
325 330 335

Val Leu Pro Asn Phe Leu Pro Tyr Asn Val Met Leu Tyr Ser Asp Ala
340 345 350

Pro Val Ser Glu Leu Ser Leu Glu Leu Leu Leu Gln Val Val Leu
355 360 365

Pro Ala Leu Leu Glu Gln Gly His Thr Arg Gln Trp Leu Lys Gly Leu
370 375 380

Val Arg Ala Trp Thr Val Thr Ala Gly Tyr Leu Leu Asp Leu His Ser
385 390 395 400

Tyr Leu Leu Gly Asp Gln Glu Glu Asn Glu Asn Ser Ala Asn Gln Gln
405 410 415

Val Asn Asn Asn Gln His Ala Arg Asn Asn Asn Ala Ile Pro Val Val
420 425 430

Gly Glu Gly Leu His Ala Ala His Gln Ala Ile Leu Gln Gln Gly Gly
435 440 445

Pro Val Gly Phe Gln Pro Tyr Arg Arg Pro Leu Asn Phe Pro Leu Arg
450 455 460

Ile Phe Leu Leu Ile Val Phe Met Cys Ile Thr Leu Leu Ile Ala Ser
465 470 475 480

Leu Ile Cys Leu Thr Leu Pro Val Phe Ala Gly Arg Trp Leu Met Ser
485 490 495

Phe Trp Thr Gly Thr Ala Lys Ile His Glu Leu Tyr Thr Ala Ala Cys
500 505 510

Gly Leu Tyr Val Cys Trp Leu Thr Ile Arg Ala Val Thr Val Met Val

515	520	525
Ala Trp Met Pro Gln Gly Arg Arg Val Ile Phe Gln Lys Val Lys Glu		
530	535	540
Trp Ser Leu Met Ile Met Lys Thr Leu Ile Val Ala Val Leu Leu Ala		
545	550	555
Gly Val Val Pro Leu Leu Leu Gly Leu Leu Phe Glu Leu Val Ile Val		
565	570	575
Ala Pro Leu Arg Val Pro Leu Asp Gln Thr Pro Leu Phe Tyr Pro Trp		
580	585	590
Gln Asp Trp Ala Leu Gly Val Leu His Ala Lys Ile Ile Ala Ala Ile		
595	600	605
Thr Leu Met Gly Pro Gln Trp Trp Leu Lys Thr Val Ile Glu Gln Val		
610	615	620
Tyr Ala Asn Gly Ile Arg Asn Ile Asp Leu His Tyr Ile Val Arg Lys		
625	630	635
Leu Ala Ala Pro Val Ile Ser Val Leu Leu Leu Ser Leu Cys Val Pro		
645	650	655
Tyr Val Ile Ala Ser Gly Val Val Pro Leu Leu Gly Val Thr Ala Glu		
660	665	670
Met Gln Asn Leu Val His Arg Arg Ile Tyr Pro Phe Leu Leu Met Val		
675	680	685
Val Val Leu Met Ala Ile Leu Ser Phe Gln Val Arg Gln Phe Lys Arg		
690	695	700
Leu Tyr Glu His Ile Lys Asn Asp Lys Tyr Leu Xaa Gly Gln Xaa Leu		
705	710	715
Gly Glu Leu Arg Thr Glu Ile Trp Ala Asn Lys Ala His Leu His His		
725	730	735
Leu His Ser His Pro Lys Asn Lys Val Val Val Ser Thr Thr		
740	745	750

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TNTTTGAAGT TTCTCCCTCT CATTCTGAG

29

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GNTTCTCCAC GTAGTTGGTT TTCCTCAGT

29

- (2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CNACATGACG TGAGCTGGTG ATCCATGAA

29

- (2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ANTTGGGCTC TGCCGTCCAG AAAGGTTTG

29

- (2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GNAGCTACGC GGAATTGCAG AGGTTTTAT

29

- (2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TNGGTGAGAG AATAGAGACT GGCTGGGAA

29

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ANGAGCCGAC CAGACGTGCA AGATGCATA

29

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ANCTGACCAG GACTCTCCTT CCACAGAGG

29

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TNTAGGCGGA AATGGTGCTG GCCATGGTG

29

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:
ANATATCCAG CCACCAACCA CAAATGAGA

29

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GCTAATTTGA GAAGAAAACA AGTAGGATTT TTGTTTTGTT TTGCATTTTG CAATATGGAG	60
GAGAAATGAT TAGACCTTAG GAAGTGCCAG TGGGTTGGTC CTTTCATGAA CATGCCATCA	120
GTAAAGCCC TGGAAACAAG GTCATACCAG AGATTTCATTG TGCCTTGTC CAACTGCAAA	180
CAATATCTGA GTGGAATATT CAAAACTTG CTTAGAAAGA AAACCTTAGG ACAGATGGCT	240
CCACTGAAGT TATTCCAAAT ATTTAATAAA TAAAGCATAC CAGGCTTTTA TAAACTCTTC	300
TAGAAGAAAA AAGTTGGAAC TTTTCCAATT CAGTTTTTCA GGCCAGTGCA ACCTTGATAC	360
CAAAACCAAT AAAACAAACA AACAAACAAA AACATAAAG CTATAGACCA AAGTCTCATA	420
GATTTAGATG CAAAATCCTA AAATTGAAAA AAAAAGTCTA GTCATATCCA TAAACTGTAT	480
CATCACCAAG AGATGTTTAT TAGGGCAATC AAAAGATGAT TTATTATTTT TTAATAAATC	540
AATGTGGCCT TCCCTTCCTC TTTCTTTTGA TTCCCCTCTT TGAGTTTTTA TGTGTCTCTT	600
TTGCCTTCCC TTCCCAGAGT GGAGGAGTTA GACCTGCATT GTGGGATGAG AGGAGTTGTG	660
GCTATGTGTC TGCTGGCACC AAGAGGGGCTG AGGGTGAGGT GTGGAAGGGA CAGGGGGAGG	720
AGATGGGCAG CATTGTTAAG AGATTGGTAC CACTGAGCAA ATATGTTGAG AATGATGATG	780
GCAAGGTTTC TCCCTGTTAG AGAAGGTATT TGTAGAAATA GGAATGAGGA GAGCTAGAAA	840
ACCTGGAGTG TGGGATTAGA ATAGAACTCA TATCTTTTAA ATACATAGGA ACAATAGAGA	900
AATTGTTGGG TGTGCCCATA TACATATATT TTGTGATTCA TTCTACCGAG AGGACATAAA	960
TGCAGTCACA GCTCAGTAAC AGTAAACACA CCAACTGCCA AGTTATTATT TCCTAAATAC	1020
TATCCACAAA AAAGGGGACC AGGGATGATT CCTAGTCGGA GATTGGGAGA AAAAGAAGAT	1080
GAGCCTGAAT CATTTTCATGT ACCTAACAGA AAGAAAATAC TCTGGCTGGG CTCAGWGGCT	1140
CATGTTTGTA ATTCTAGCAT GTTAGGAGGT CGAGGTGGGT GTGTTGCTTG AGCCCAGGAG	1200

TTTGAGACCA GCCCAGGCAA CATGGCAAAA CTGTCTCTAC AAAAAATATA AAAGTTAGCC 1260
 AGGCGTGGTG GCATGCGCCT GTCGTCCGAG ATACTCGGGA GGCAGAGAGG TGGGAGGATC 1320
 ACTTGAGCCT GGGAGATTGA GACTGCATCG AGCTGTGGTC ATGCCACTGC ACTCCAGCCT 1380
 GGAGGACAGA GTGAGACCCT GTCTCAGGAA AAAAAAAAAA AAAAA 1425

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Ile Tyr Tyr Phe Leu Lys Asn Gln Cys Gly Leu Pro Phe Leu Phe
 1 5 10 15
 Leu Leu Ile Pro Leu Phe Glu Phe Leu Cys Val Ser Phe Ala Phe Pro
 20 25 30
 Ser Gln Ser Gly Gly Val Arg Pro Ala Leu Trp Asp Glu Arg Ser Cys
 35 40 45
 Gly Tyr Val Ser Ala Gly Thr Lys Arg Ala Glu Gly Glu Val Trp Lys
 50 55 60
 Gly Gln Gly Glu Glu Met Gly Ser Ile Val Lys Arg Leu Val Pro Leu
 65 70 75 80
 Ser Lys Tyr Val Glu Asn Asp Asp Gly Lys Val Ser Pro Cys
 85 90

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CGCACCCAGC CGCGCCGGCG AGGACATGGG CAGCCGCGGC GCGCCCACCC CCCGCGCCGA 60
 TGTGAATTAT TAAAAAGAAA ATGGCCCAAC GGAGCACTGT ATTTCTTCT CGTGTCACCA 120
 AGGAAAGGTA TAATATATGG AAAATATGCA TCTAAGGCGA GTGAGAACCA TGCCCCGACA 180
 CAGCCAGTCC CTGACCATGG CACCATACTC ATCTGTAAGC CTCGTGGAGC AGCTGGAAGA 240
 CAGGATCCTC TGCCATGAGA AAACCACCGC CGCCCTCGTA GAGCACGCCT TTCGGATTAA 300
 AGATGACATT GTCAACAGTT TGCAGAAAAT GCAAAACAAA GGGGGAGGTG ACCGCTTGGC 360

CAGGCTTTTC TTGGAGGAGC ATATCAGAAA CATAACTGCC ATAGTGAAGC AACTTAATCG	420
GGATATCGAG GTACTCCAGG AGCAGATTCG TGCTCGGGAC AACATTAGCT ATGGAACATA	480
TTCTGCCTTA AAGACCCTGG AGATGCGCCA GCTCTCCGGT TTGGGAGATC TTCGAGGAAG	540
AGTGGCAAGA TGTGATGCCA GCATAGCTAG ACTTTCTGCA GAGCACAAAA CGACCTATGA	600
GGGGCTCCAG CACTTGAACA AAGAACAGCA GGCTGCCAAA CTTATCTTGG AAACGAAAAT	660
CAAAGATGCA GAGGGACAGA TTTCTCAGCT TTTGAACAGA GTGGACTTGT CAATATCAGA	720
GCAGAGCACC AACTGAAGA TGTCTCACAG AGACAGTAAC CACCAGCTTC AGCTTTTGGA	780
CACTAAATTT AAAGGTACAG TTGAGGAAGT CAGTAACCAG ATATTATCTG CACGGAGTTG	840
GTTGCAACAG GAACAAGAAC GGATAGAAAA AGAGCTTTTA CAGAAAATTG ATCAGCTTTC	900
CTTGATTGTT AAGGAAAACA GTGGAGCCAG TGAAAGGGAT ATGGAGAAGA AGCTCAGCCA	960
GATGTCAGCC AGGCTTGACA AAATAGAAGA GGGTCAAAAG AAGACTTTTG ATGGTCAGAG	1020
AACAAGGCAA GAAGAGGAGA AGATGCACGG GCGAATCACC AAGCTGGAGT TACAGATGAA	1080
CCAGAACATC AAGGAAATGA AAGCAGAAGT TAATGCTGGG TTTACAGCCG TCTATGAAAG	1140
CATAGGATCC CTCAGGCAAG TTCTCGAGGC CAAGATGAAG CTGGACAGGG ACCAGCTACA	1200
GAAGCAAATC CAGCTGATGC AGAAGCCAGA GACCCCATG TGAAGGGAGC TGGGACAAGG	1260
TCCTAAAAGA CAGTTTTGCC AGTGGGGCTA GGAGCCGGAT ACCTCTGTAG CCAGGCCATC	1320
GCTGCATTCA GGATTGTTCC ATCCATGGCG TGCATGTGCC AAGAAATGTG TTTTATGGG	1380
TCTAAATGTT TACCTGAGT CTTGAAAATA CTCTTTTGTT AAAAGTATGA AATACAGTTT	1440
TTACCAGTTT ATTTCACTTC TCTAAATTCA ATGGAAATCC CCCGCCCTGG ATTTTGAAAG	1500
GCTTTTATCT TCTTCATTTT ACGAATGGAA AGACGACAAT TTTTCTTCAA TGCTTGATGC	1560
ACTAATGAAG ACTGTTTACT ATTTTGAAAA ATGTCATGGG GATTTTTTTT TAATTAAGAA	1620
ACTAATGAAT CATCACAGGA ATGTGTTGCT CCTCACCTA AATTAAGAGA ATGTCCCACT	1680
AGATTAGACT TCAACCTTTG AGTCCAATTT GGATTTTATT ATCGTTGTCT ATGCACTTCT	1740
TATATTGGTT ATCTTCTTGT AAATCTTCTG TCTTTTGTA GGGGAAAGGA TTTAACATTT	1800
AGAATAAACC CCACCATTTA TGTAATGGAA ATAGTTTAAA AATTGCTAAC TGCCATGTGG	1860
ATTGCAAATT AAATGGAAAC TTATTTAGAT AACGTAAGGC TCAATATCTG CGTTGACCAC	1920
CTAGATATTA CAGGTTTTAA TATTTAAAAC TATTTTGTAA TTATCCACAA CCTGTATAGT	1980
GATAGCCATA TATTTAATAA TGGAATGGTG GTTAACAGTC TATTTACTGC ACAATTAATT	2040
GTTCACTAAT CAAATAGAAT GTGGTAATTT TTCAGACTTT ATGATCTGTT TCCAAAATTG	2100
GCACAAAGTG CTAGGGTTTA TATACACTTA TCGTAACTGT ATTTTGTGC CTTGGTTTTA	2160

TCATGTCAAT GCACTGTACT CTGTAAAAGT TTTGCAGACA AAATAGAAAG TATGATAATC	2220
CGTCAGAAGT ATGATGTAAA ACTGGAATCC TCTGTATTTT TTAAATGTTC TAAAAATTTT	2280
ATCGCTGTTA AGGTATTAAT CATTCAAGTAT TACTAATGGA ATAGAAATTC ATACTTTTGT	2340
ATGGACAACA AATTGATATT GCATTTATAG CACTGTAAGA AACTTTCATC TTGAGCAACT	2400
TTGTAGATGA TGGGTGTTTT ATTTTCAATC GCCATATTTG ATCAGTCATT GAAAATTGGC	2460
CCCAGTGCTG TTTGTTCATC TCTGTATGTA AAAACTGACA GTGAGACACA ACTTTCTGAA	2520
CTGTGAGGGT GTCCCAGGAA AAAGAAAAAC AGGAATACTT TAACAATTAA AAAGAAAAAA	2580
ATGTTTTTTG TTTGCCAAGG ACTCAGGAAA ATAAAAAGCA TTTTCTATTT TTAGGACAAA	2640
TCACAAATGA AGTGTCTAAC TGGCTATTAC TGTTTACCCA TATAAAATAT GCTGCTAAAG	2700
TACATATTTT GCTGTCAATG GCTTGACAAT TTTTTTTTTC AAATTGAGGAC ATGAGAGGTT	2760
ATATAGGGAC TATATTATCC AACACATATT TTCTTATTTT GCCACAAATT TCCACTTAAC	2820
AAATAAAAAA AGGCGAATGC TGTTTTGCAA AAAAAAAA	2859

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met	Glu	Asn	Met	His	Leu	Arg	Arg	Val	Arg	Thr	Met	Pro	Arg	His	Ser
1				5					10					15	
Gln	Ser	Leu	Thr	Met	Ala	Pro	Tyr	Ser	Ser	Val	Ser	Leu	Val	Glu	Gln
			20					25					30		
Leu	Glu	Asp	Arg	Ile	Leu	Cys	His	Glu	Lys	Thr	Thr	Ala	Ala	Leu	Val
		35				40						45			
Glu	His	Ala	Phe	Arg	Ile	Lys	Asp	Asp	Ile	Val	Asn	Ser	Leu	Gln	Lys
	50					55					60				
Met	Gln	Asn	Lys	Gly	Gly	Gly	Asp	Arg	Leu	Ala	Arg	Leu	Phe	Leu	Glu
65				70					75					80	
Glu	His	Ile	Arg	Asn	Ile	Thr	Ala	Ile	Val	Lys	Gln	Leu	Asn	Arg	Asp
			85						90					95	
Ile	Glu	Val	Leu	Gln	Glu	Gln	Ile	Arg	Ala	Arg	Asp	Asn	Ile	Ser	Tyr
		100						105					110		
Gly	Thr	Asn	Ser	Ala	Leu	Lys	Thr	Leu	Glu	Met	Arg	Gln	Leu	Ser	Gly
		115					120					125			
Leu	Gly	Asp	Leu	Arg	Gly	Arg	Val	Ala	Arg	Cys	Asp	Ala	Ser	Ile	Ala

130	135	140
Arg Leu Ser Ala Glu His Lys Thr Thr Tyr Glu Gly Leu Gln His Leu		
145	150	155 160
Asn Lys Glu Gln Gln Ala Ala Lys Leu Ile Leu Glu Thr Lys Ile Lys		
	165	170 175
Asp Ala Glu Gly Gln Ile Ser Gln Leu Leu Asn Arg Val Asp Leu Ser		
	180	185 190
Ile Ser Glu Gln Ser Thr Lys Leu Lys Met Ser His Arg Asp Ser Asn		
	195	200 205
His Gln Leu Gln Leu Leu Asp Thr Lys Phe Lys Gly Thr Val Glu Glu		
	210	215 220
Leu Ser Asn Gln Ile Leu Ser Ala Arg Ser Trp Leu Gln Gln Glu Gln		
	225	230 235 240
Glu Arg Ile Glu Lys Glu Leu Leu Gln Lys Ile Asp Gln Leu Ser Leu		
	245	250 255
Ile Val Lys Glu Asn Ser Gly Ala Ser Glu Arg Asp Met Glu Lys Lys		
	260	265 270
Leu Ser Gln Met Ser Ala Arg Leu Asp Lys Ile Glu Glu Gly Gln Lys		
	275	280 285
Lys Thr Phe Asp Gly Gln Arg Thr Arg Gln Glu Glu Glu Lys Met His		
	290	295 300
Gly Arg Ile Thr Lys Leu Glu Leu Gln Met Asn Gln Asn Ile Lys Glu		
	305	310 315 320
Met Lys Ala Glu Val Asn Ala Gly Phe Thr Ala Val Tyr Glu Ser Ile		
	325	330 335
Gly Ser Leu Arg Gln Val Leu Glu Ala Lys Met Lys Leu Asp Arg Asp		
	340	345 350
Gln Leu Gln Lys Gln Ile Gln Leu Met Gln Lys Pro Glu Thr Pro Met		
	355	360 365

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 933 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGCTTCGGAG ACCGTAAGGA TATTGATGAC CATGAGATCC CTGCTCAGAA CCCCCTTCCT	60
GTGTGGCCTG CTCTGGGCCT TTTGTGCCCC AGGCGCCAGG GCTGAGGAGC CTGCAGCCAG	120
CTTCTCCCAA CCCGGCAGCA TGGGCCTGGA TAAGAACACA GTGCACGACC AAGAGTACGT	180

ATTCAGCCCCG GGCTGTGGTC CAGTGGCCTC CCCATCATCT GCAGCTGAGC CAGCGGCAAG 240
 GGCATGCTCA GTCCTCCTTT CCTTCTTCCT GTTTCTATGG CTCCTTGACA TTCTTCAAGG 300
 ATGATTCTTA TTCCTTATTG CCACCTATAA GTCAGGTATT CTTTTTTCAT CATTGTATCA 360
 CAGGTGGAAG ATCTTTAGGC CCAAATGGGG CACATTACTT GTCTGAATCC GGTCTCTCCT 420
 TTTTTTCACC ACAGACAGAC ACACACACAT ACAAATAGAC ACACAGGTAC ACATACACAG 480
 TCATAGTAGC AGAATCCAGA AAATAGCTAA GGTTTCTTGA CTATAACAAG ACCTTTTTTTA 540
 AATCAACACA TTCAAACATT GAATCATTTG TTGCAGCTTT TGTCTTGGGC CAGTTAGCCT 600
 CACGCATTAT ACTCGGTTAT CCTTTGTTTT TAAGGCTGGG TGCAGTGGCT CACACCTGTA 660
 ATCCCAGTGC TTTGGGAGGC TGAGGCAGGT GGATTACTTG AGCCCAGGAA TTCGAGACCA 720
 GCCTAGGCAA TATAGGGAAA ACCTGTCTCT AYTAATAAAT TGCAATAAAT TAGCTGGATG 780
 TGGCAGTACA TGCCTATGGT CCCAGCTACT TGGGGGGCTG AAGTGGGAGA ATCAAMTGAG 840
 CTTGGGAAGT TGAGGCTACA ATGAGCCAAG ATCAGCTCC TGCACTCCAG CCTGGGTGGC 900
 AGAGTGAGAC CCTGTCTCAA AAAAAAAAAA AAA 933

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met Thr Met Arg Ser Leu Leu Arg Thr Pro Phe Leu Cys Gly Leu Leu
 1 5 10 15
 Trp Ala Phe Cys Ala Pro Gly Ala Arg Ala Glu Glu Pro Ala Ala Ser
 20 25 30
 Phe Ser Gln Pro Gly Ser Met Gly Leu Asp Lys Asn Thr Val His Asp
 35 40 45
 Gln Glu Tyr Val Phe Ser Pro Gly Cys Gly Pro Val Ala Ser Pro Ser
 50 55 60
 Ser Ala Ala Glu Pro Ala Ala Arg Ala Cys Ser Val Leu Leu Ser Phe
 65 70 75 80
 Phe Leu Phe Leu Trp Leu Leu Asp Ile Leu Gln Gly
 85 90

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2956 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGTGTGTGGT GGTTTAAGAA TGTATATCAT AGGGTCAGGT GGCCTGGGTT CATTCCCCAG	60
CTACGTAACC TTTCTATGCC TGAGTTTCCT CATCTATAAA ACAAGGATAA TAATAGTGTG	120
TACTTCTTAG GATTGTTTTG GAGACTCATA AATGAGAAAT ACGTGAAAAA CTCCCTCAAG	180
GCAGTGCTTG ACACATAATG AGCACTCAGT TATCATGGTC ATCATGGTCA TCATCACTGC	240
TACCACCACT GCTGCTGCTA TTACCACTCT ACCTCTTCCC CCTGAAACTC TAATCACTTA	300
CCCTAGAAAC AGTTAAATTA CACTTCAGTG GGAAGGATCT CAGATTTCTT AATGGCACCT	360
GCATTTATAT AATGTTGATA TTGCACGTTT CTAGAAAACA TATCAAGAAG AAACCAAAAT	420
GTGTTTCTGT ACTTTGTAAA CCTGTACAAT AGTTAGAGAT TAGAGGACCT TTATAATCTA	480
CTACTAATTA CTGTGAAAGT AAACATTGTT TAATATACCA GTTCTTAAAG AAATATTTTG	540
TCTAGTCATT AATATTCTAG TTCATCTCAA AGCTTCCATT TGACAATTTA AAATTACTTA	600
AATTTTAATA TTAAAGGAAA CAGTTTTCCT GATTCTCATG AAAGTTCCTA TTTGCACTGA	660
AGATGACTAA ACCTTTTAGT CATAGTTTGA GAAGAATTGG CTTTTTTATA GCCATTTTAT	720
TTACATATGG GTACTGCATA GCAAAGGCAG CAGATTAGCC CTGTTTGTTT TGCAGGGATG	780
AAAGGTAGCA TTCCCAGAGA TTAAGTTGTT CTGCTATTC CCATTCTCTG CTACATTGTC	840
CTACATTCTT TGGTCCTTTC TATTATTTGT TTCTTTGGTG GAATCCCCTT GTTGCTTATG	900
GCTGGATATT GTTATTCAGC AGATGAATCA CAAGTTTAGC CTGAGGGCCC TAAAGCATCA	960
GAAATAAATT AGAGCCGAGC AAAGTTTAAC TTCTCTGGAA CTTGCACCTT TAGTTTCCAT	1020
GTATTTCTGG AACCAAGATA TTTCAAAGGC TTACTTTATT TCAGACACCT ATTATCTTCA	1080
AGTCACAGAT AACTATTGAT TCTGTAAAGT GTTTCAAAGA TTTTGTCCA CTAGACATTT	1140
TTAAATTTGT TCAACTCCTC CTCATCATTT TAGAAATTAT TTCTGTTAGG TAAAATTAAA	1200
ACTAACAATG TATTTTAGTT TATTTTCTA ATGATACCAG TCACCTTTCG GGGCTAACTA	1260
AACATTTTGT GCAGCATTCT CTTAGTTTAC ATCCTCCTTT CTTTCAGTCT TCCTGTTTAT	1320
TAAGGCTGTC CTGTAGCAAA CAAAAGAGTG ACTCATGTGA AAAGTATTTT AACTGCTCTA	1380
ATATATCTGA GGAAGAATAA CTTTCTAAAT TAAAGTAATG TATTTTATTA AATATTAAAA	1440
TGCATTTTTT GGCTATTCAT TTCTGTATGT AAAAGAAAAG TTAACCTTAT GGTGTTATGC	1500
AAAATATGCT AAATTTAGAT TTTAGAGCAA TATATAGGGA GATATGTCAC AAATTTCTAC	1560
ATTTTGGTTA AATTATTAGT ATTTTCTTAT ATTCAAATGT GCCTTGATAT TTAAATAATA	1620

TACTGAATGC AGAATTTATG TTATGTGAAC CATTATGGAA AATGTTAATG TTAACAAAAT	1680
GAGGTGTATT GACTTTTCAA CAATGTAAAT TAAAGATGGT ACATCTACTG TTTAAGGGCA	1740
GAGGAATTAA AAGAGTATAG ATACTGAAAT GTATCACTTA CTAGTAGTGT GGCTATAATC	1800
AAATTAATTA ATCTCTCTCT AGGCTTTAGC TTCCTCATCT TAGTTTGTTT AGGCTACTGT	1860
AACAAAATAA CATAGATTAT GTACTTTTAA ATGACAGAAG TTTATTCGGC ATGGTTTGGG	1920
AGACTAGGAA GTCTAAGATT AAAGAACCAG CAAATTTGGT GTCTGATGAG GACCCATTCC	1980
TTTGTTTACA GATGATGCCT TCTCATTGTG TTTTCAAATG TTAGAAGGAG CTAGCTAGCT	2040
TTCTGGGGTC TCTTTTGTA AGGCACTAAT CCCAGTCATT AGGGCAAATT GGCTCCTACA	2100
GGCCCCACCT ATCTCCTAAT ACCATCACCT TGAGGATTAA GATTTCTACA TATGAATGAA	2160
GCAGGTGTTG TAGAAGGTCA GTCAGTTAGA CCATAGCACC ATCTGTAAAA TTGAATAGTA	2220
ATTTACTGCC TCATTGGATG TCAGGATTAA AGGAGATAAG ATTTTATTAG TTACTAGTTA	2280
CCATAGTGGT TTTTTTTTTT CACTATAATG TTCGTTTTTT TGTTCATGC TTGTACCTTC	2340
AACATTTCTT TCCATTTGAA TACTTCTTTT GTCTCCTGTA GGCCTGTCTG TCCACTTAGG	2400
TGTAAGATGT GTTTTTGTGT CAGGAATGAT GGTGCAATGC TAATGTTCCA TTGCCCTATT	2460
TGGCAATACT CTGATCATT ACTATAAAGA ATAACACCAG TGTTAACTAA CTCTCCTTGC	2520
CTGACAGTAG TGCTGCCACT ATTCCTTGTT TCTGTGGTAA TAGATGAGGT TTGTATGGTC	2580
CTGTTATTCC AGCCTCCAGA CACCATTCCA GATCAACTGG TGCCYTCWAC GCCCCGAAG	2640
TGTATGGGGC CTCAGGTGAA GGATGAGWAC ATTTTCACTA TCATCTGGCA TTCATCTCAG	2700
ATTTTATCCT TTTCAGTTTC CATTAAATAA TATTCATGTT TTAAAATTGA TTTTTATTA	2760
TTTAAATTTA ATTTGTTGGA GAATAAACTT TTTTTTTTCT TTTCTCCCAA GTAACGTTTT	2820
CCCCTTTAGC AACTGTATTG AGCATTTTTT TCACTGGTAT ATGGACATTT TTTTGTATAA	2880
CCTGTTGTGT CATTTTAAAA TATAGAATTG TTTTATGTT CTCATCTTTG TATATATGTT	2940
TAAAAAATAA AAAAAA	2956

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met	Thr	Lys	Pro	Phe	Ser	His	Ser	Phe	Arg	Arg	Ile	Gly	Phe	Phe	Ile
1									10					15	

Ala Ile Leu Phe Thr Tyr Gly Tyr Cys Ile Ala Lys Ala Ala Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AATCGGGAAA AAAAGCCATG TATTCTTTTCG TTTCTCTCTA AAAGAAGAAA AATATAATTT	60
AAAAATACAT TCGGTATTTT CTAAAACAAT AAATTTATAG TGTTAATATT CATAGGGTCA	120
ATCAAAATGA AGCTTCTCCT TTGGGCCTGC ATTGTATGTG TTGCTTTTGC AAGGAAGAGA	180
CGGTTCCCCT TCATTGGTGA GGATGACAAT GACGATGGTC ACCCACTTCA TCCATCTCTG	240
AATATTCCTT ATGGCATACG GAATTTACCA CCTCCTCTTT ATTATCGCCC AGTGAATACA	300
GTCCCCAGTT ACCCTGGGAA TACTTACACT GACACAGGGT TACCTTCGTA TCCCTGGATT	360
CTAACTTCTC CTGGATTCCC CTATGTCTAT CACATCCGTG GTTTTCCCTT AGCTACTCAG	420
TTGAATGTTC CTCCTCTCCC TCCTAGGGGT TTCCCGTTTG TCCCTCCTTC AAGGTTTTTT	480
TCAGCAGCTG CAGCACCCGC TGCCCCACCT ATTGCAGCTG AGCCTGCTGC AGCTGCACCT	540
CTTACATCCA CACCTGTAGC ATCTGAGCCT GCTGCAGGGG CCCCTGTTGC AGCTGAGCCT	600
GCTGCAGAGG CACCTGTTGG AGCTGAGCCT GCTGCAGAGG CACCTGTTGC AGCTGAGCCT	660
GCTGCAGAGG CACCTGTTGG AGTGGAGCCA GCTGCAGAGG AACCTTCACC AGCTGAGCCT	720
GCTACAGCCA AGCCTGCTGC CCCAGAACCT CACCCTTCTC CCTCTCTTGA ACAGGCAAAT	780
CAGTGAAATT CTCTAGAAGA GTACCATGGG TTCATTTCTA TACTGATGCA GAAATAAGTG	840
AAATCTACAA AAGTTTTCTT TCTTTTCCAA AGACTATTTT ATTCTGTAGT ATTCAGAGTA	900
TTCATCTCAC TACATAGATT TGTTTGTGGT AGTTATTTCC TTGGACTTAA TTTATATTGA	960
AAAAACATTG ATAATTAAAT AAATAAAATA GATAATTTAG ACCAATGGTG ATAAGGTCTG	1020
GATGAAACT ACGCTATGGA GGACTGAAAT GGCAATCATT CAGCCTAGCC TGGAGTCTGA	1080
TTATACAGCT ACTATAGGAT GATGTTAGTA TTGGTTTTGA GTGCAATAGG TTTTTTCTA	1140
AACAAACATA TTTTGTAGTC AATGAACTTT TTGTCACAAA ACAGTAAAAC ATCTGTGTTT	1200
AACCTATGGT AAACAACATG TTAATGAACT ATGCTATCCA TGACTTAATG GACAGTTCAA	1260
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1320
AAAAA	1325

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

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Met Lys Leu Leu Leu Trp Ala Cys Ile Val Cys Val Ala Phe Ala Arg
 1           5           10           15
Lys Arg Arg Phe Pro Phe Ile Gly Glu Asp Asp Asn Asp Asp Gly His
          20           25           30
Pro Leu His Pro Ser Leu Asn Ile Pro Tyr Gly Ile Arg Asn Leu Pro
          35           40           45
Pro Pro Leu Tyr Tyr Arg Pro Val Asn Thr Val Pro Ser Tyr Pro Gly
          50           55           60
Asn Thr Tyr Thr Asp Thr Gly Leu Pro Ser Tyr Pro Trp Ile Leu Thr
65           70           75           80
Ser Pro Gly Phe Pro Tyr Val Tyr His Ile Arg Gly Phe Pro Leu Ala
          85           90           95
Thr Gln Leu Asn Val Pro Pro Leu Pro Pro Arg Gly Phe Pro Phe Val
          100          105          110
Pro Pro Ser Arg Phe Phe Ser Ala Ala Ala Ala Pro Ala Ala Pro Pro
          115          120          125
Ile Ala Ala Glu Pro Ala Ala Ala Ala Pro Leu Thr Ser Thr Pro Val
          130          135          140
Ala Ser Glu Pro Ala Ala Gly Ala Pro Val Ala Ala Glu Pro Ala Ala
          145          150          155          160
Glu Ala Pro Val Gly Ala Glu Pro Ala Ala Glu Ala Pro Val Ala Ala
          165          170          175
Glu Pro Ala Ala Glu Ala Pro Val Gly Val Glu Pro Ala Ala Glu Glu
          180          185          190
Pro Ser Pro Ala Glu Pro Ala Thr Ala Lys Pro Ala Ala Pro Glu Pro
          195          200          205
His Pro Ser Pro Ser Leu Glu Gln Ala Asn Gln
          210          215

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(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TGCGGGCTCA CANGAANAGT CTCACCTCAG TGCCAAGGGG TGTCAGAGAT GCTCACTGCC	60
CTCCTCTCCT TGGGGTTGCA TGNAGGCATG ATGGCGCTTG GCCGTGGCAG GGTAAGGAAC	120
CGGCGACNGA GGCCCATCAC GTGTTACAT GCTCTCCTGC GTCNGTGCTT GGGAGATATG	180
GACTGTCNTG TCCTTAGACC ACATTTATNT CAAGGCAAGG GGAGC	225

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GGTTCAAAAT GAGGCAAAGA TAGGAAAGTG CTTCTTACAG ATAATTTTCA AGGCCAGTGA	60
CTGGAGAGAG GGGTAGGTCT GTCAATCGAG TGCTTGCTGA CTGCACATAT CACAGGGCGT	120
GTGACGACTG CTGGGAGAGG AAAGCGAGAC ATCATTCCAA CCCTCCAGAA GCTAAAGATC	180
CTGGAACTCA AGGGGAAAAC TAACGTAAGT GCGAAAGCGA ACAAGCAAAC ATGTCTCTCA	240
CGGGGCAGGC AGGCTGTCTGG GGTACAGAGC TGGGATCTGG GAAGGAACAG AGAGGGCCGC	300
TCAGGGAGAG GAAGCACAGT GCCACCGGAG GCACGCACTC AGCAGGCACT CGCAGGCTGG	360
GCAGAGGTAG AGAAGCAGCG CTGCACAGGC AGGCAGCTGA CCCAGGGCTC TTAGAGCCGG	420
GCAGGAGAGC TGGTGTGGGA CCTGGGAGGA GGACAGGAGC CTTCAAAGCA GCACCGCCTG	480
ATTGCAGCCA GGAGGGTAGC ATCAAGGAAG ATGGAAGTGC GGCCAGGCCA CAT	533

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met	Ser	Ser	Thr	Gly	Gln	Ala	Gly	Cys	Arg	Gly	Thr	Glu	Leu	Gly	Ser
1				5				10						15	
Gly	Lys	Glu	Gln	Arg	Gly	Pro	Leu	Arg	Glu	Arg	Lys	His	Ser	Ala	Thr
			20					25					30		

Gly Gly Thr His Ser Ala Gly Thr Arg Arg Leu Gly Arg Gly Arg Glu
 35 40 45
 Ala Ala Leu His Arg Gln Ala Ala Asp Pro Gly Leu Leu Glu Pro Gly
 50 55 60
 Arg Arg Ala Gly Val Gly Pro Gly Arg Arg Thr Gly Ala Phe Lys Ala
 65 70 75 80
 Ala Pro Pro Asp Cys Ser Gln Glu Gly Ser Ile Lys Glu Asp Gly Thr
 85 90 95
 Ala Ala Arg Pro His
 100

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TAGGCAGTCA TCTTTGTAAA CCTCCACTGG TGCTGGCTGC GTTTAGAACA TACTCCATAT	60
AAAACAGGCC CTGGGATTAC AGGCATGAGC TACCGTGCCT GGCCCCCTTT TTTTAAATTA	120
CAGAGAAATA AGTTACACCT TAGTATCAGA TATTAATTTT CTTCAAGTGT CAGGCAATTA	180
GTATTTAGAA AGCTCTTGTC ATGAGATGGC TCTGGGATGT GATGATGATT GTTGGGATTG	240
AAAAAATGGT AGTATCATGG AGAGATCATA ATAAATTCTT AGTATTAAAA GTGGTTTTGC	300
TTTCAGTTAG GGAGAAAAAT TAGATTGTAC TATTTTTCCT CTATGATTTC CTTCAAGTTAT	360
CTTCCAAATG TTGTTTTTTC CCCACAGCCC CCTTAACATT GTTCTCTATG CACTTCTCAA	420
TACATTTTCA TTTGTTTCTC AAAAAAAAAA AAAAAAAAAA	458

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TTTTTTTTTT TTTTGTAGA GACAGGGTCT TGCCATTTTG CCCAGGTTGG TCTCAAACCTT	60
CTGAGCTCAG GCTATCTGCC CACCTTGGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC	120
CACTGTGCCC GGCCTGTATT GTTTTAAGTT ACACTTATTC CTTTAAAAAT TCAGAATTTG	180

TTAAGCATTT AAAACAAATT CATAAATTAA AACCTCCTTG AGATACCATT TACCATGTAG 240
 TTTGATGAAC ATAATACATG GTGCATTACA TTGGCAAAAG CAGTGGGGAA AAAGATGCTT 300
 TTATAAATGT CTGGTGGGAG TTAAATTGTG TAACTTCTAT TACACTTTTG TAATAGCTAC 360
 CAAAATATGT TATTTCTATC TACCTCTCTC TCTCTGACTC AACAGTTCCA TTTCTAGGTT 420
 TTGTGTTGTG GATATTCTTG AACATTGTGA AATGTATACA GGGAGGCTTC ACAGCAGCAC 480
 TGTTTGTTTC AAATGATTTG AAAACAACCT CTCCATAAAC GAGATAGGCT AAATCAAGCA 540
 TGGCACACCT ATACAATGGA TCGGGCCATT AAAAAGAACA AGGCAGCTCA TATGCATCAA 600
 TATAAAAAGG TCTATAAACT ATACTATCAA ATGAAAATAG CAAGATGCTA CCATTTATAT 660
 TAAAAAGAGG ACAAATATT AATATATTCA TGGTTGCTTG TCTATGTGGA ATATTTCTGG 720
 ATATATACAT AAGAAGTTAC ATTGGTTACC TATGGGCAGG TTACTACTGG GTGGCTTGTG 780
 GGTGAGGGCA GGAAGAGCTT ACTTTCCATG GTAAACCTTT TTGTATATTT TGCAGCATTC 840
 AAAAATTCTA ATTTAAAGTT TATTTTAGAA AAATGCCCCC ATGTATACAA GTGATTTCCA 900
 AGTTCCTCCT TCAATATTTT TAATGATTAT GGAACACACT GAACTTCTTT TTTATTATTC 960
 TAGCTGTGAA CTCTGTCTGC TGTCTACATG CACATATATA ATCTATGTAA TATTTAAATT 1020
 TATATCCTTT ATATGTCAGT TGGGTGGTGA GTAAAAGAAA AATATATTTT TATCAGCAAA 1080
 CTTGGTAAAT TGTTGAGGTT TCTGATATAG TCAGAGGTAG TTGCTTATCA CAACATTAGG 1140
 TAAGTTTTTA AARACACCTA TTAAAACAC ACTGATGTAT ATATATATTG GTCTGTTTTT 1200
 ATGCTGCTGA TAAAGACATA TCCAAGACTG GGAAGAAAAA GAGGTTTAAT TGGGCTTATA 1260
 GTTCCACATG GCTGGGGAGG CCTCAGAATC ATTGCGGGAG GCAAAAGGCA CTTCTTACAT 1320
 GGCAGTGGCA AGAGAAAAAA AAAAAAAAAA 1350

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Leu Pro Phe Ile Leu Lys Arg Gly Gln Asn Ile Asn Ile Phe Met
 1 5 10 15
 Val Ala Cys Leu Cys Gly Ile Phe Leu Asp Ile Tyr Ile Arg Ser Tyr
 20 25 30
 Ile Gly Tyr Leu Trp Ala Gly Tyr Tyr Trp Val Ala Cys Gly
 35 40 45

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

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TCGGGACACT ACATGAAGTC CTGAAAATAA CAGAGAAACT GTTATATCTT TTTAATGATT      60
TATTTGCAAG TATTGAGGTT GACCTGAAAA ACAATGAAAC ACATGAACAC ACTTCCGATT      120
TTCTCCTCGC TGATTAGCTT CCTGCCTGCT GTCAGTGCTG GACGAAGTGC TATAACTACT      180
TTATGTAACA TTACAGAACA GCTAGAGGTC CTGGGGTAAG AGAAAAAAG CACATCACAA      240
CAAATGTGAA AGCCTTCATT ATTACACGTT CCAGTTTGTC TCGCTGTGTA GGCATAAGCT      300
AATGGTTTAT TTTCAGAAAG CTGCCTGAAA CGTTGCTTTG TATTCTTCTA GGAAGAACTT      360
TAATTCCTCC TGAGGAACTC TACTTTCTGA GCCAACTGC TAATTTTCTG CGGAACTGTC      420
TAGAAGATCA TTCAAGAGAC CCTGCAGTTG CACTTTCTCG TAAAGTTAA AAAAAAAAAA      480
AAAAAAAAAG GTTTTCCCG GCCTTTGAAC ATTTTGCCTA TGAGAGTTTT GCATATATTT      540
TATACTTGAG TAGACAACTT TAATAATCCA TATTTATACT ATCGCAGAAG TAAGCATTTG      600
GCAAACGTTT AGCCATTAGC ACTCATTTAA CCCTGTTAGC AATATTCTTT TGAAAAAAGT      660
GCCAGTCCTT ATGTGATAAA CTAAGAAGCC CATTGAATAT AAAANTGTGT NGGACTGAAA      720
CNGTGACCTT ATATTATTGC TAAGGGAATA TGAGATTAAC TTCCTACAGG GGCCANAACC      780
ANANAAAGGC TTCCAGCAAC TTCGATNAAA NTANTTTGGC CACATNTCAA GCCAATTGTT      840
TGTAATATTT ATGTACCTTT TTCATAACTG GAATTGCCAA ATAAGCATGG AGATCTAAAT      900
GRAAAAAAAA AAAAAAAAAA AAAGCGGCCG CAGGTCTAGA ATTCAATCGG AAAAAACAAA      960
GAGAAGAAAC ATACTGCCCC ATCTTGTTTG CATGAACTC TAGAATCTGG TGTTTCTCTA     1020
TTTATCTGCT CCCTCTTTGC CTACCTTGGN ATTTCTTTTT TTTTTCTTT GTAACATATGG     1080
TTTTTACCTA AAGTTTAAAC TTTTATTAT TATTTTCTCT CTAAATTCTT GCTAGTTAAT     1140
AACATTATTA ACTTCAAGAT TTTAGAAGAG CAGTGATGAT AGTAATGATC GATAACTAGA     1200
CTATCGAGTT TCAGAAGAAA CTTCCAAGTA TATATAATGT TTGACATAGC CTTTATTTCT     1260
ACAAATCTAC TACCTGTAAA CTAACATTTT AAAATACCTG TATATGGCTG GGTGTGGTGG     1320
CTTACACCTG TAATCCCAGC AGTTTGGGAG CCTGAGGTGG GCAGATTGCT TGAGCCCAGG     1380
AGTTGGAGAC AAGCCTGGAC AAAATAGACC TCTCTCTACA AAAAGTACAA AAAATTGGCT     1440
GGGTGTGGTG GCACACGCCT GTGGTCCCAG CTACTCGGGA GGCTGAGGTG GGAGGATTGC     1500

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CTGAGCCCGG GAGATGGTGG TTGCAGTGAG CTGAGATCAC CCCATTGCAC TCCAGCCTGG 1560

ATAACAGAAT AAGATGCTGT CTTAAAAAAA AAAAAAAA 1598

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Lys His Met Asn Thr Leu Pro Ile Phe Ser Ser Leu Ile Ser Phe
1 5 10 15

Leu Pro Ala Val Ser Ala Gly Arg Ser Ala Ile Thr Thr Leu Cys Asn
20 25 30

Ile Thr Glu Gln Leu Glu Val Leu Gly
35 40

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CATGGCGTCC AGGTCTAAGC GCGTGCCGT GGAAAGTGGG GTTCCGCAGC CGCCGGATCC 60
CCCAGTCCAG CGCGACGAGG AAGAGGAAAA AGAAGTCGAA AATGAGGATG AAGACGATGA 120
TGACAGTGAC AAGGAAAAGG ATGAAGAGGA CGAGGTCATT GACGAGGAAG TGAATATTGA 180
ATTTGAAGCT TATTCCTAT CAGATAATGA TTATGACGGA ATTAAGAAAT TACTGCAGCA 240
GCTTTTTCTA AAGGCTCCTG TGAACACTGC AGAACTAACA GATCTCTTAA TTCAACAGAA 300
CCATATTGGG AGTGTGATTA AGCAAACGGA TGTTTCAGAA GACAGCAATG ATGATATGGA 360
TGAAGATGAG GTTTTTGGTT TCATAAGCCT TTAAATTTA ACTGAAAGAA AGGGTACCCA 420
GTGTGTTGAA CAAATTCAAG AGTTGGTTMT ACGCTTCTGT GAGAAGAAGT GTGAAAAGAG 480
CATGGTTGAA CAGCTGGACA AGTTTTTAAA TGACACCACC AAGCCTGTGG GCCTTCTCCT 540
AAGTGAAAGA TTCATTAATG TCCCTCCACA GATCGCTCTG CCCATGTACC AGCAGCTTCA 600
GAAAGAAGT KCGGGGGCAC ACAGAACCAA TAAGCCATGT GGGAAAGTGCT ACTTTTACCT 660
TCTGATTAGT AAGACATTTG TGGAAGCAGG AAAAAACAAT TCCAAAAAGA AACCTAGCAA 720

CAAAAAGAAA GCTGCGTTAA TGTTTGCAAA TGCAGAGGAA GAATTTTCT ATGAGAAGGC 780
AATTCTCAAG TTCAACTACT CAGTGCAGGA GGAGAGCGAC ACTTGTCTGG GAGGCAAATG 840
GTCTTTTGAT GACGTACCAA TGACGCCCTT GCGAACTGTG ATGTTAATTC CAGGCGACAA 900
GATGAACGAA ATCATGGATA AACTGAAAGA ATATCTATCT GTCTAACCCA TTTCCAATGG 960
ACAGTGATGG GCTTGTTTTT GTAAAATTAC CAGAAAAGTC AGTGGAGATT TACTGAAAAA 1020
CTCAGACTTT ATTCAAGATTA AGTTCCTCTA CAAAAGTAG GGTCTGTCC CATGTGTYTC 1080
TGACACATTT ACAAATACC AGTTTTTTAA AATTTTGGTC AAATTATGAG TGGTTGATTT 1140
AAAAACTTTT CCAAGAAGAA GAAAGCATG GAGTAGTAAT TTAAAGAACT CAATAAAAC 1200
TTCTATTTTT TATTTTAAAA TAATAAAAAA AAAAAAAAAA AAAAAAA 1257

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Ala Ser Arg Ser Lys Arg Arg Ala Val Glu Ser Gly Val Pro Gln
1 5 10 15
Pro Pro Asp Pro Pro Val Gln Arg Asp Glu Glu Glu Glu Lys Glu Val
20 25 30
Glu Asn Glu Asp Glu Asp Asp Asp Ser Asp Lys Glu Lys Asp Glu
35 40 45
Glu Asp Glu Val Ile Asp Glu Glu Val Asn Ile Glu Phe Glu Ala Tyr
50 55 60
Ser Leu Ser Asp Asn Asp Tyr Asp Gly Ile Lys Lys Leu Leu Gln Gln
65 70 75 80
Leu Phe Leu Lys Ala Pro Val Asn Thr Ala Glu Leu Thr Asp Leu Leu
85 90 95
Ile Gln Gln Asn His Ile Gly Ser Val Ile Lys Gln Thr Asp Val Ser
100 105 110
Glu Asp Ser Asn Asp Asp Met Asp Glu Asp Glu Val Phe Gly Phe Ile
115 120 125
Ser Leu Leu Asn Leu Thr Glu Arg Lys Gly Thr Gln Cys Val Glu Gln
130 135 140
Ile Gln Glu Leu Val Xaa Arg Phe Cys Glu Lys Asn Cys Glu Lys Ser
145 150 155 160

Met Val Glu Gln Leu Asp Lys Phe Leu Asn Asp Thr Thr Lys Pro Val
165 170 175

Gly Leu Leu Leu Ser Glu Arg Phe Ile Asn Val Pro Pro Gln Ile Ala
180 185 190

Leu Pro Met Tyr Gln Gln Leu Gln Lys Glu Leu Xaa Gly Ala His Arg
195 200 205

Thr Asn Lys Pro Cys Gly Lys Cys Tyr Phe Tyr Leu Leu Ile Ser Lys
210 215 220

Thr Phe Val Glu Ala Gly Lys Asn Asn Ser Lys Lys Lys Pro Ser Asn
225 230 235 240

Lys Lys Lys Ala Ala Leu Met Phe Ala Asn Ala Glu Glu Glu Phe Phe
245 250 255

Tyr Glu Lys Ala Ile Leu Lys Phe Asn Tyr Ser Val Gln Glu Glu Ser
260 265 270

Asp Thr Cys Leu Gly Gly Lys Trp Ser Phe Asp Asp Val Pro Met Thr
275 280 285

Pro Leu Arg Thr Val Met Leu Ile Pro Gly Asp Lys Met Asn Glu Ile
290 295 300

Met Asp Lys Leu Lys Glu Tyr Leu Ser Val
305 310

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCGGTCCTGC CACACAAGCT GGGCGGCGGA GGCCACGCAG CCGGGCCTTC TTCTCTCTGG	60
GACCCTCCGC CAGCGCATAG CCGCAGGCCG GTGTGACTTC TGCACCCTCG GTTCTGAGGG	120
TACGGTGACC CCTAGTGGGC AGTTTGCAA ATGTGATTCC TTCTTCCCAA CTCCCCATCC	180
CCCCTTCCCT TCCCGTCACG TCCTGTTTGG GGGTTAATTC GGTTTTTTCT CTGTTGCATC	240
GCGCCTACTG TGC GTGTGCG ATARCGTGTG TGGGGGTGAG AGTTTGTTTT CTGGAATGGT	300
AGGTGCTGGG AGGAGGAGTT TGATGGAGGG CTTCTGGCT GCTTCTGGCC CTCACCTCGT	360
GGAGGCCTTC ACAGAGACCC TGTGGGCCCT GGCCCTGTGC TGGCACTGTG CCAGTCATGA	420
GGCAGCTCTG ATCACTTCCC CACTGTGGAA ACAGGACTGA CCCAGCCTTC AGTGTGGGCT	480
GCTGAAGCTA TCCTCCTCAG GCCTCAGGGA TGACCTCCTG CCTGAGCCTC TCACAGGCTG	540
GCTGTGGGCC AGTTTCATCT GCTTTCCTGT TGGGGGTCCC GGGCCTCTGC TGTCTTGAC	600

CCACTGGTGT TCTGTGCAAG GCTTCTTCCC ATTCACCAAG TGCACACCTT GCATCTGCCG 660
 CTCGGCATGC ACCAGTTCCA CACACCATCC CATTTTACAG ACAAGGACGC TGAGGCCTGC 720
 AGCAGCAGTG TGA CTTGCTC AAGGTCCAGT GAGTGACCTC ATTCCCCAGA AAAGGCTCCT 780
 CCCACACCAG AGTACAGCCT GGGTAGGGGG AAAATCAGTT CTTTCAGCTA CCACCCATCC 840
 AACCTTTGGG CCTATGTGAA AAGAAAGGAA CTAAGCTGGG TGTGTTCTGT CTGGACCTGG 900
 GGAGGCCCCCT GAAGGCAAAG AGGGAAACTG TCCCAGCTGT TCTGTCCTAG GGGAGGGGGA 960
 CATAGCCCTA GCAGGAGCTC CCAGCCCCTC TTGGCACTCT GACACACAAG TACACCCATC 1020
 TGGGGCCCGC TTTGCCACGA AGAGCTGGGC AGGCCTGCAG GGTGTGGGGA AGGAGGACAC 1080
 AACCTCAAGA AAGGAAGCGT GAACCCAGG GAACAGCGGG TCCCTTCCCT CCTCAGACAC 1140
 AAGCCACCTC AGCTTGTGGC TCTTGGCCCC CAGCCCCACC AACCCACCTG TTCATTTATT 1200
 CAACAGACAA TGACAGCTGA TATTTATTGG ACATTTGCAC CATGCCAAGC ATTCGGCTTG 1260
 GATTATCCCA TTTGTTTCTC ACAGCCGGTA TTTATTGTCT GCTCCTCTGT GCCAGGTGCT 1320
 GTGCTCTGGG CAGGGGCACT GCATGGGCTG CCTGCCCTGG TGGAGCTTGT GGTCTGATGG 1380
 GTGAGGCTGA CCAAGCCCA CCCATTGCC AACAGGGCCA GGGCAAGAGT ACACACAGGG 1440
 GCCTCATACC ATATGTCTAA ATATTTAAAA GTTATCAATC AAGCTAACA CTGTAAATA 1500
 AAATATGTTC TATTCTCCTA CTTTGAAAAA AAAAAAAAAA AAAA 1544

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met Pro Ser Ile Arg Leu Gly Leu Ser His Leu Phe Leu Thr Ala Gly
 1 5 10 15
 Ile Tyr Cys Leu Leu Cys Ala Arg Cys Cys Ala Leu Gly Arg Gly
 20 25 30
 Thr Ala Trp Ala Ala Cys Pro Gly Gly Ala Cys Gly Leu Met Gly Glu
 35 40 45
 Ala Asp Pro Ser Pro Pro His Cys Gln Gln Gly Gln Gly Lys Ser Thr
 50 55 60
 His Arg Gly Leu Ile Pro Tyr Val
 65 70

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CNATGCAGGTC TAACTCCTCC ACTCTGGG

29

- (2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TNAGTTTGGTG CTCTGCTCTG ATATTGAC

29

- (2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GNCATCAATAT CCTTACGGTC TCCGAAGC

29

- (2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GNAAATAGGAA CTTTCATGAG AATCAGGA

29

- (2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ANACAATGCAG GCCCAAAGGA GAAGCTTC

29

- (2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GNTTGCTTGTT CGCTTTCGCA CTTACGTT

29

- (2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ANTGGTAGCAT CTTGCTATTT TCATTGTA

29

- (2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

TNGGAAGTGTG TTCATGTGTT TCATTGTT

29

- (2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GNCCTCGTCCT CTTTCATCCTT TTCCTTGT

29

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ANCACCTGGCA CAGAGGAGCA GACAATAA

29

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGCGAGCCTT TGAGGGGAAC GACTTGTCGG AGCCCTAACC AGGGGTATCT CTGAGCCTGG 60
TGGGATCCCC GGAGCGTCAC ATCACTTTC GATCACTTCA AAGTGTAAGG GGGGCCCTAC 120
TGACCCTTGG AATTTAGGGG GGCTACCCTA GGCGGCATCC ACAACAGAGA GAATTCCTT 180
GGAGAGGGGA CCCTGGTGCT CGGCTGTCCC TCTCATCCGC GTAGAAAGTC CCTCATCTGG 240
GGGCTCCCGA ACTCAGCCCT CTCACATTGT GGCCGGCTTT ACTGACCCTC ACAGACCCAG 300
GCTGGGCCCT CCCGATAGAG GCCAGCCAAA GGTTCACTCA GCCTCTCTTT CAAGGCTGGT 360
GTATCTCTAA ATCTTAGACC CTCCTCCGTT ACCGTCAGCC AGGTGGGATG CCCACGTTT 420
GGAGAGAAAC CGTTCTGAGG AACCCGGGCC TCTGGGTCCC AGCTGGCTCT CCGGCCCCCA 480
GGTTATGTAT TCTGGGTGG CCACAAACAG TGGAATTCTA GGCACTCCCG GGACAGGGTG 540
GGACTGCTGT CCTCATTCAT GCAACCAGCA AATATTCACG GCACCTTGTT TGTGCCAGAC 600
AGCAGACCGA GGACACGGTT GTTACCAAGA CCAGGCTGTT GCCTTGGAAG AGCCCAGAGC 660
GTGTCAAGGG AGACAGCCAC ATCAGGCCAG AAATACATGA CAGCTGGATT AGCCCTGGGA 720
GAGGGAGGCC CAGATGTGGG AGCTCAGGGG AGGTGCAGCT CAACGTGGAG TTTGGAGGAG 780
GCTACCTTGA CTTTGAATG CCAAGTGGGA GCCAGCCAGA TGAAAGGGGT TAAAACTAA 840
TATTTATATG ACAGAAAGAAA AAGATGTCAT TCCGTAAAGT AAACATCATC ATCTTGGTCC 900
TGGCTGTTGC TCTCTTCTTA CTGTTTTTGC ACCATAACTT CCTCAGCTTG AGCAGTTTGT 960
TAAGGAATGA GGTACAGAT TCAGGAATTG TAGGGCCTCA ACCTATAGAC TTTGTCCCAA 1020
ATGCTCTCCG ACATGCAGTA GATGGGAGAC AAGAGGAGAT TCCTGTGGTC ATCGCTGCAT 1080
CTGAAGACAG GCTTGGGGG GCCATTGCAG CTATAAACAG CATTACAGAC AACACTCGCT 1140
CCAATGTGAT TTTCTACATT GTTACTCTCA ACAATACAGC AGACCATCTC CCGTCCTGGC 1200
TCAACAGTGA TTCCCTGAAA AGCATCAGAT ACAAATTGT CAATTTTGAC CCTAACTTT 1260

TGGAAGGAAA	AGTAAAGGAG	GATCCTGACC	AGGGGGAATC	CATGAAACCT	GTGATATTCT	1320
TGCCCTTTAC	AATACAGCAC	TGAAGCCAGG	ACATGCAGCT	GCATTTTCAG	AAGATTGTGA	1380
TTCAGCCTCT	ACTAAAGTTG	TCATCCGTGG	AGCAGGAAAC	CAGTACAATT	ACATTGGCTA	1440
TCTTGACTAT	AAAAAGGAAA	GAATTTCGTAA	GCTTTCCATG	AAAGCCAGCA	CTTGCTCATT	1500
TAATCCTGGA	GTTTTTGTG	CAAACCTGAC	GGAATGGAAA	CGACAGAATA	TAACTAACCA	1560
ACTGGAAAAA	TGGATGAAAC	TCAATGTAGA	AGAGGGACTG	TATAGCAGAA	CCCTGGCTGG	1620
TAGCATCACA	ACACCTCCTC	TGCTTATCGT	ATTTTATCAA	CAGCACTCTA	CCATCGATCC	1680
TATGTGGAAT	GTCCGCCACC	TTGGTTCCAG	TGCTGGAAAA	CGATATTCAC	CTCAGTTTGT	1740
AAAGGCTGCC	AAGTTACTCC	ATTGGAATGG	ACATTTGAAG	CCATGGGGAA	GGACTGCTTC	1800
ATATACTGAT	GTTTGGGAAA	AATGGTATAT	TCCAGACCCA	ACAGGCCAAAT	TCAACCTAAT	1860
CCGAAGATAT	ACCGAGATCT	CAAACATAAA	GTGAAACAGA	ATTTGAACTG	TAAGCAAGCA	1920
TTTCTCAGGA	AGTCCTGGAA	GATAGCATGC	GTGGGAAGTA	ACAGTTGCTA	GGCTTCAATG	1980
CCTATCGGTA	GCAAGCCATG	GAAAAAGATG	TGTCAGCTAG	GTAAAGATGA	CAAAGTCCCC	2040
TGCTCGGCAG	TCAGCTTCCC	AGACGAGACTA	TAGACTATAA	ATATGTCTCC	ATCTGCCTTA	2100
CCAAGTGTTT	TCTTACTACA	ATGCTGAATG	ACTGGAAGAA	AGAAGTCTGA	TGGTAGTTTC	2160
AGCTAGCTGG	TACAGATAAT	TCAAAACTGC	TGTTGGTTTT	AATTTTGTA	CCTGTGGCCT	2220
GATCTGTAAA	TAAAACCTTAC	ATTTTTCAAT	AGGAAAAAAA	AAAAA	A	2271

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met 1	Ser	Phe	Arg	Lys 5	Val	Asn	Ile	Ile	Ile 10	Leu	Val	Leu	Ala	Val 15	Ala
Leu	Phe	Leu	Leu 20	Val	Leu	His	His	Asn 25	Phe	Leu	Ser	Leu	Ser 30	Ser	Leu
Leu	Arg	Asn 35	Glu	Val	Thr	Asp	Ser 40	Gly	Ile	Val	Gly	Pro 45	Gln	Pro	Ile
Asp	Phe 50	Val	Pro	Asn	Ala	Leu 55	Arg	His	Ala	Val	Asp 60	Gly	Arg	Gln	Glu
Glu 65	Ile	Pro	Val	Val 70	Ile	Ala	Ala	Ser	Glu	Asp 75	Arg	Leu	Gly	Gly	Ala 80
Ile	Ala	Ala	Ile	Asn 85	Ser	Ile	Gln	His	Asn 90	Thr	Arg	Ser	Asn	Val 95	Ile
Phe	Tyr	Ile	Val 100	Thr	Leu	Asn	Asn	Thr 105	Ala	Asp	His	Leu	Arg 110	Ser	Trp
Leu	Asn	Ser 115	Asp	Ser	Leu	Lys	Ser 120	Ile	Arg	Tyr	Lys	Ile 125	Val	Asn	Phe
Asp	Pro 130	Lys	Leu	Leu	Glu	Gly 135	Lys	Val	Lys	Glu	Asp 140	Pro	Asp	Gln	Gly
Glu 145	Ser	Met	Lys	Pro 150	Val	Ile	Phe	Leu	Pro	Phe 155	Thr	Ile	Gln	His	

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
GCCGACCGAA GAGGCTGGAC ATGACACCAG TGGCATATCA CGGCCATGGG GTCTCAGCAT 60
TCCGCTGCTG CTCGCCCCCTC CTCCTGCAGG CGAAAGCAAG AAGATGACAG GGACGGTTTG 120
CTGGCTGAAC GAGAGCAGGA AGAAGCCATT GCTCAGTTCC CATATGTGGA ATTCACCGGG 180
AGAGATAGCA TCACCTGTCT CACGTGCCAG GGGACAGGCT ACATTCCAAC AGAGCAAGTA 240
AATGAGTTGG TGGCTTTGAT CCCACACAGT GATCAGAGAT TGCGCCCTCA GCGAACTAAG 300
CAATATGTCC TCCTGTCCAT CCTGCTTTGT CTCCTGGCAT CTGGTTTGGT GGTTCCTTC 360
CTGTTTCCGC ATTCAGTCCT TGTGGATGAT GACGGCATCA AAGTGGTGAA AGTCACATTT 420
AATAAGCAAG ACTCCCTTGT AATTCTCACC ATCATGGCCA CCCTGAAAAT CAGGAACTCC 480
AACTTCTACA CGGTGGCAGT GACCAGCCTG TCCAGCCAGA TTCAGTACAT GAACACAGTG 540
GTGAATTTTA CCGGGAAGGC CGAGATGGGA GGACCGTTTT CCTATGTGTA CTTCTTCTGC 600
ACGGTACCTG AGATCCTGGT GCACAACATA GTGATCTTCA TGCGAACTTC AGTGAAGATT 660
TCATACATTG GCCTCATGAC CCAGAGCTCC TTGGAGACAC ATCACTATGT GGATTGTGGA 720
GGAAATTCCA CAGCTATTTA ACAACTGCTA TTGGTTCTTC CACACAGCGC CTGTAGAAGA 780
GAGCACAGCA TATGTTCCCA AGGCCTGAGT TCTGGACCTA CCCCCACGTG GTGTAAGCAG 840
AGGAGGAATT GGTTCACCTA ACTCCCAGCA AACATCCTCC TGCCACTTAG GAGGAAACAC 900
CTCCCTATGG TACCATTTAT GTTCTCAGA ACCAGCAGAA TCAGTGCCTA GCCTGTGCC 960
AGCAAATAGT TGGCACTCAA TAAAGATTG CAGAATTTAA TACAGATCTT TTCAGCTGTT 1020
CTTAGGGCAT TATAAATGGA AATCATAACG TGGTTCTAGG TTATCAAACC ATGGAGTGAT 1080
GTGGAGCTAG GATTGTGAGT GACCTGCAGG CCATTATCAG TGCCTCATCT GTGCAGAAGT 1140
GGCAGCAGAG AGGGACCATC CAAATACCTA AGAGAAAACA GACCTAGTCA GGATATGAAT 1200
TTGTTTCAGC TGTTCCCAAA GGCCTGGGAG CTTTTTGAAG AGAAAGAAAA AAGTGTGTTG 1260
GCTTTTTTTT TTTTGTAGAA GTTAGAATTG TTTTACCAA GAGTCTATGT GGGGCTTGAT 1320
TCACCCTTCA TCCATTGGCT GGAACATGGA TTGGGGATTT GATAGAAAAA TAAACCCTGC 1380
TTTTGATTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA 1425
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg
 1             5             10             15

Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu
 20             25             30

Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser
 35             40             45

Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln
 50             55             60
```

Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg
65 70 75 80

Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu
85 90 95

Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu
100 105 110

Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln
115 120 125

Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn
130 135 140

Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln
145 150 155 160

Tyr Met Asn Thr Val Val Asn Phe Thr Gly Lys Ala Glu Met Gly Gly
165 170 175

Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu Ile Leu Val
180 185 190

His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile Ser Tyr Ile
195 200 205

Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr Val Asp Cys
210 215 220

Gly Gly Asn Ser Thr Ala Ile
225 230

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CTTCCAAAGA GCGACTCTTA CTGTTTCTCA TGGTGAGAAG ACAATATTTG CTTTCTCTTT 60

TTCCTTTCTT CCGGATGAGA GGCTAAGCCA TAATAGAAAG AATGGAGAAT TATTGATTGA 120

CCGTCTTTAT TCTGTGGGCT CTGATTCTCC AATGGGAATA CCAAGGGATG GTTTTCCATA 180

CTGGAACCCA AAGGTAAAGA CACTCAAAGA CAGACATTTT TGGCAGAGCA TAGATGAAAA 240

TGGCAAGTTC CCTGGCTTTC CTTCTGCTCA ACTTTCATGT CTCCCTCCTC TTGGTCCAGC 300

TGCTCACTCC TTGCTCAGCT CAGTTTTCTG TGCTTGGACC CTCTGGGCCC ATCCTGGCCA 360

TGGTGGGTGA AGACGCTGAT CTGCCCTGTC ACCTGTTCCC GACCATGAGT GCAGAGACCA 420

TGGAGCTGAA GTGGGTAAGT TCCAGCCTAA GGCAGGTGGT GAATGTGTAT GCAGATGGAA 480

AGGAAGTGGA AGACAGGCAG AGTGCACCGT ATCGAGGGAG AACTTCGATT CTGCGGGATG	540
GCATCACTGC AGGGAAGGCT GCTCTCCGAA TACACAACGT CACAGCCTCT GACAGTGGA	600
AGTACTTGTG TTATTTCCAA GATGGTGA CTCTATGAAAA AGCCCTGGTG GAGCTGAAGG	660
TTGCAGCACT GGGTTCTAAT CTTCACGTCG AAGTGAAGGG TTATGAGGAT GGAGGGATCC	720
ACCTGGAGTG CAGGTCCACC GGCTGGTACC CCCAACCCCA AATACAGTGG AGCAACGCCA	780
AGGGAGAGAA CATCCCAGCT GTGGAAGCAC CTGTGGTTGC AGACGGAGTG GGCCTATATG	840
AAGTAGCAGC ATCTGTGATC ATGAAAGGCG GCTCCGGGGA GGGTGTATCC TGCATCATCA	900
GAAATTCCCT CCTCGGCCTG GAAAAGACAG CCAGCATTTT CATCGCAGAC CCCTTCTTCA	960
GGAGCGCCCA GCCCTGGATC GCAGCCCTGG CAGGGACCCCT GCCTATCTTG CTGCTGCTTC	1020
TCGCCGGAGC CAGTTACTTC TTGTGGAGAC TACAGAAGGA AATAACTGCT CTGTCCAGTG	1080
AGATAGAAAG TGAGCAAGAG ATGAAAGAAA TGGGATATGC TGCAACAGAG CGGGAAATAA	1140
GCCTAAGAGA GAGCCTCCAG GAGGAACTCA AGAGGAAAAA AATCCAGTAC TTGACTCGTG	1200
GAGAGGAGTC TTCGTCCGAT ACCAATAAGT CAGCCTGATG CTCTAATGGA AAAATGGCCC	1260
TCTTCAAGCC TGCCTGATTT TTCCTGCATG GGAAGAGCGC ACATGTNGCC CTGAGGTTCC	1320
CTTCCCAGGA CNGCTCCAGG ATCGAGATCA CTGTGAGTGG TTGTGGAGTT AAGACCCCTA	1380
TGGACTCCTT CCCAGCTGAT TATCAGAGCC TTAGACCCAG CACTCCTTGG ATTGGCTCTG	1440
CAGAGTGTCT TGGTTGAGAG AATAACGTTG CAGTTCCCAC AGGGCATGTG ACTTTGAAAG	1500
AGACTAAAGG CCACACTCTG TTAATAATGG GGCACATATG TGTTCCCACC CCACAAATGT	1560
GATAAGTGAT CGTGCAGCCA GAGCCAGCCT TCCTTCAGTC AAGGTTTCCA GGCAGAGCAA	1620
ATACCCTAGA GATTCTCTGT AATATTGGTA ATTTGGATGA AGGAAGCTAG AAGAATTACA	1680
GGGATGTTTT TAATCCCACT ATGGACTCAG TCTCCTGGAA AAGGATCTGT CCACTCCTGG	1740
TCATTGGTGG ATGTTAAACC CATATTCCTT TCAACTGCTG CCTGCTAGGG AAAACTGCTC	1800
CTCATTATCA TCACTATTAT TGCTCACCAC TGTATCCCCT CTACTGGGCA AGTGCTTGTC	1860
AAGTTCTAGT TGTTCAATAA ATTTGTTAAT AATGCTGAAA AAAAAAAAAA AAAAAAAAAA	1920
A	1921

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val
1 5 10 15

Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser
20 25 30

Val Leu Gly Pro Ser Gly Pro Ile Leu Ala Met Val Gly Glu Asp Ala
35 40 45

Asp Leu Pro Cys His Leu Phe Pro Thr Met Ser Ala Glu Thr Met Glu
50 55 60

Leu Lys Trp Val Ser Ser Ser Leu Arg Gln Val Val Asn Val Tyr Ala
65 70 75 80

Asp Gly Lys Glu Val Glu Asp Arg Gln Ser Ala Pro Tyr Arg Gly Arg
85 90 95

Thr Ser Ile Leu Arg Asp Gly Ile Thr Ala Gly Lys Ala Ala Leu Arg
100 105 110

Ile His Asn Val Thr Ala Ser Asp Ser Gly Lys Tyr Leu Cys Tyr Phe
115 120 125

Gln Asp Gly Asp Phe Tyr Glu Lys Ala Leu Val Glu Leu Lys Val Ala
130 135 140

Ala Leu Gly Ser Asn Leu His Val Glu Val Lys Gly Tyr Glu Asp Gly
145 150 155 160

Gly Ile His Leu Glu Cys Arg Ser Thr Gly Trp Tyr Pro Gln Pro Gln
165 170 175

Ile Gln Trp Ser Asn Ala Lys Gly Glu Asn Ile Pro Ala Val Glu Ala
180 185 190

Pro Val Val Ala Asp Gly Val Gly Leu Tyr Glu Val Ala Ala Ser Val
195 200 205

Ile Met Lys Gly Gly Ser Gly Glu Gly Val Ser Cys Ile Ile Arg Asn
210 215 220

Ser Leu Leu Gly Leu Glu Lys Thr Ala Ser Ile Ser Ile Ala Asp Pro
225 230 235 240

Phe Phe Arg Ser Ala Gln Pro Trp Ile Ala Ala Leu Ala Gly Thr Leu
245 250 255

Pro Ile Leu Leu Leu Leu Ala Gly Ala Ser Tyr Phe Leu Trp Arg
260 265 270

Leu Gln Lys Glu Ile Thr Ala Leu Ser Ser Glu Ile Glu Ser Glu Gln
275 280 285

Glu Met Lys Glu Met Gly Tyr Ala Ala Thr Glu Arg Glu Ile Ser Leu
290 295 300

Arg Glu Ser Leu Gln Glu Glu Leu Lys Arg Lys Lys Ile Gln Tyr Leu
305 310 315 320

Thr Arg Gly Glu Glu Ser Ser Ser Asp Thr Asn Lys Ser Ala
325 330

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```
AATGGTTCCA GCCTTAATGG AGAAGCCAGT TTCTTTTTTC TTGTTGTTTT ATTGTTTTTA 60
AGCCTCTCTC TGGTTTTTCAG TAGAGTTTGA CCTTAAATAT CATCTTTGAT TACTATTGGT 120
GTCCTTGTA TAAAGGTCTT TGCAAAAGTT TGAGTGCAAG TTTTAAGCTA AAAACACGTT 180
TTTAACTTT CACAAATTTT GTAAGATGAC AATAGCATTC TGTAACATAG ACATTATGGT 240
AATAGTGATT TTCTCTCCAT CCCTATTTTG TCCAGCGATT TCCAAGTTAT AAGACGTGAA 300
TAAGACTAAC CGCTCACTTC CACCAGCAGC TGACCTGGTG GGCTTTTGAG TTCAAAGAGT 360
CATTTCTTCA TCTTACCTCC AGCACTGCAG GGCCGTGTGA CCTGCAGAG CCTTGTTTCT 420
CATTGATGAA AGGAGCTCAT GCCTCATGAA GCCACTGGTA AGGGCCATGG AGCTCACGGG 480
CCATCAAGCT TCCTTCCCAT CACTTGTGGG TGAATTGAC ATTACCCGAT GAGCTCTTCC 540
TGGGGTCACC TGGGAGGGAG TGGCCCATGG GTGGTATGAC AAAATCTCAT AGTCAGTCTT 600
TGCAGTTTTT TCCACAGGTA AAATGAGATT TTGGAAAATT TTCATTGTGTT TGTATTGTGTC 660
CCAAGGTGAG TCTTACATAT TTTGAGCAAC AAAACGAAGA TCATTATGAA AATGTCCTTA 720
TGGAAGCACT CTAGGGCCAT TGCTCATTTT TATGAGTCCT CGTGCTAAGT CCCTGAGTAC 780
TGTGGCTCAT GTCTTAGCTG GCTAAATCAC AGTCAAAATT CTCTTCTTAA GCCTCAAAAT 840
AAGCTGCTGA TTATACTGCC TGTTGGCCAG ACTAATCAAA TACATTTGAT GTTTTAGCTG 900
ACTCCAGATA CTTTTCTTTC CTCCTCCTTG GTTCTTTAAC TGTCATCCCA GATCTGCGAC 960
ATGCAATAAG GAAAACAGAG TCAGGGAGGA AGTAGGATTC CTTTGTCTGC TAGGAACCAC 1020
GTTAGCTTTG GATTGTCCAT AGAATGCACC CTTAACAGTT CTTGGAAAAT GGATGATATT 1080
TGGTTCCTGC CCCATGTTCA GTGTTCTTTG GCAGCTGCAA AGCATATCCT AGCTAGAATC 1140
CTTATCGTCT TGAAGTTCAT CAAAGATTTT GAACAGTCAT GGTGGAGATA CAACCTAAGT 1200
ACATTCATGC CCATTGAGAC AATCCTTTTG TTTGAGCGAC GGAAGGAGGA ATAAACACAT 1260
GAATGTATTT TATTGAATCC CAGAGACCCT GAAACACCAA GACTCATTAA TATATGCATA 1320
CATGGATGGC AGAATAATAA ACCTCACCTG ACCTGTCAGT GTACTCTCAG TTTTAAAGGT 1380
TCTCCCAAAA CAGGGAAACT GAAAAATACT TGGGCAGAAA GAAAATATCA TCAAATAACA 1440
CCTATTTCTT TTCAGCTATA GAGATGGCTG GATATCAAAA GCACCACGGG AGCTTTGCAA 1500
TTTGCTGCTC TTTTCAGCCC TCAGCTTGAC TCTCAGTTT CAAGAGGGAG AAAATGAATG 1560
TTTCCCAGCA TTCTCTGTCC TTTGCTCCAA AGAAGAGAGC AGGTGTTGGC TTCCAAACCT 1620
TCCGTATTTT CTTATTGCTG TTAGGGGGAT CAACTGCATG TTTCTTGAGG GAAAAGGGTG 1680
GCTCACTGAC CTAATTGAAG GCATTCTCTC AGTGGAAGCT GGGCAAGAGA ATCCAGGGAT 1740
TTCTTTTGCA GGTTCCTGCG CAGTGCCCTT GCCATCAAGC TGCCTAAAAT GTGAATATTG 1800
CTTCCCTGCG TTTCAAGAGT GGTAAATATT GGGCAAGTGG TGGAGGATCT AAAAAAAAAA 1860
AAAAA 1865
```

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Asn Val Ser Gln His Ser Leu Ser Phe Ala Pro Lys Lys Arg Ala

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2094 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:137:

-106-

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Met Ser Ala Arg Thr Gln Phe Ile Cys Leu Ile Gly Phe Ile Lys Leu
 1           5           10           15
Leu Glu Asn Phe Ser Ile Cys Tyr Phe Phe Pro Leu His Leu Leu Ser
          20           25           30
Asn Ala Pro Asn Glu Phe Val Thr Gln Ser Gln Leu Phe Pro Ser Leu
          35           40           45
Ser His Cys Phe Leu Leu Ser Pro Thr His Arg Ile Asn Met Lys Leu
          50           55           60
Ser Ser Arg Ser Val Met Ile Ser Leu Arg Lys Asn Phe
          65           70           75

```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

AAATTCAACA TAAACCCAAA TCTGTACTTC TCCAGAGGAG CAGCTCTGAG GTAGAAATTA 60
CAACGATGAA AAGAGCACAA CGTACAAAAC CAAGAAAGAG TCTGTTGTGT GAAGGGTCAT 120
TCGATGAAGA AGCTTCTGCA CAGTCCTTTC AGGAAGTGTT AAGTCAATGG AGAACCGGAA 180
ATCATGATGA CAACAAGAAA CAGAATTTAC ATGCAGCAGT AAAAGACTCA TTGGAAGAAT 240
GCGAAGTACA GACTAATCTG AAAATTTGGA GAGAACCACT TAATATTGAA CTTAAAGAAG 300
ACATTCTATC CTATATGGAA AAATTATGGC TTAAAAAACA CAGGAGAACT CCACAAGAGC 360
AACTTTTTAA AATGCTACCA GATACGTTCC CACATCCACA TGAAACCACT GGTGATGCAC 420
AGTGTTCTCA AAATGAAAAC GATGAAGATA GTGATGGTGA GGAGACCAA GTACAACACA 480
CAGCTCTTTT ATTGCCAGTA GAAACATTAA ACATAGAGAG ACCTGAACCA TCTCTAAAGA 540
TAGTCGAACCT GGATGATACT TATGAAGAGG AATTTGAAGA AGCAGAAAAT ATTGTGCCTT 600
ACAAAGTTAA ATTAGCTGAT GCAGACAGTC AACGAAGTTG TGCTTTTCAT GATTGTCAGA 660
AGAATAGCTT TCCATATGAA AATGGCATCC ATCAACATCA TGTTTTCGAT AAGGGAAAGA 720
GAGACTTCTT AAATCTTTGT CTGAGAAACA GCTATACTTA TTATAAAGAT AATTCAAAAG 780
CAGAACTTTC AAACACAGAT TTTGACAACA TCGTGGATCC TGATGTGTAT TCTTCTGACA 840
TTGAAAAAAT TGAGGAAAGC ACCTCCTTTG AAAGAAATTT AAAGGAGAAA AATATAGGTT 900
TAGAAAGTAA TCAAAAGTCT GATGATTCCT GTGTATCACT TGAAAGCAAG GACACTTTGC 960
TAGGTAGAGA TTTAGAAAAA GCTCCCATTG AGGAGAAATT ATCTCAAGAC ATCAAAGAAT 1020
CCTTGGAATT GAGCAATCTG TATAAGAGGC CAAGCTTTGA AGAATCAAAA ACTACAAAGT 1080
CATCACTGTT GTTACAAGAA ATAGCCTGCA GAAGTAAGCC TATAACAAAA CAATATCAAG 1140
GACTTGAGAG ATTCTTTATT TTTGATACAA ATGAAAGACT CAACTTACTT CCTTCTCATC 1200
GTTTAGAATG CAACAATTCC AGTACTAGGA TTACACTTGC AGAAGACAGA GAATGGATTTC 1260

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CAGACCATAG CTTAAGTGAA TATGCTGATA ATGCAATTGT CTTGGGTGTT CTGCAGGGTG 1320
 CTCAGAGTCC ATCATCAAGT AGAAAACAGC AAAAGATGGG TCAGAAATCA CAGAGACCTT 1380
 CAACAGCAAA TTTTCCACTT TCCAACCTCTG TTAAAGAAAG CTCCAGTTGC CTTTCATCCT 1440
 CTCATCCTCG ATCAAGAAGT GCAGCTGCTC AATCATCATC TAGAGCTGCT TCTGAAATTT 1500
 CAGAAATTGA ATATATTGAT ATTACTGACC AGAATGAGCT TTCCTTAGAT GACACTACTG 1560
 ATCAACATAC TTTAGACAAAT TTGGAAAAAG AATTACAAGT GCTGAGATCT CTTGCAGATA 1620
 CTTCAGAAAA GCTTTACAGC TTAACCTCAG AAGAGTTCCC AGATTTTCAGC AGCCAATCAC 1680
 TGAATATAAG TCAGATTTCC ACAGATTTCC TTAAGACCTC ACATGTGAGG GGTCCCTGTG 1740
 GAGTTGAGGA ATTGAGCTGT TCTGGAAGAG ATACCAAAT TCAGTCTTTG CTGTCACTTT 1800
 CTGAGAGCAG TACAGATGAG GAGGAGGAAG ATTTTCTCAA CAAGCAACAT GTCATCACAC 1860
 TACCGTGGTC AAAGAGTACT TAAAGATTAT TTGTTCATTA CTGTTTCCAT TTTGTACCCA 1920
 GAGTAAAGCA AACAACAGT AAAAGTAACC AAGTGATTAC CTATCCAAGT GCTGGAGATT 1980
 TTGATTACTA ATGTCTTTGA TGTTTCAAGG CTACAAACTA ATAAAAGTAA AATTATAAGT 2040
 TCAAAAAAAA AAAAAAAA AAAAAAAA 2069

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met Lys Arg Ala Gln Arg Thr Lys Pro Arg Lys Ser Leu Leu Cys Glu
 1 5 10 15
 Gly Ser Phe Asp Glu Glu Ala Ser Ala Gln Ser Phe Gln Glu Val Leu
 20 25 30
 Ser Gln Trp Arg Thr Gly Asn His Asp Asp Asn Lys Lys Gln Asn Leu
 35 40 45
 His Ala Ala Val Lys Asp Ser Leu Glu Glu Cys Glu Val Gln Thr Asn
 50 55 60
 Leu Lys Ile Trp Arg Glu Pro Leu Asn Ile Glu Leu Lys Glu Asp Ile
 65 70 75 80
 Leu Ser Tyr Met Glu Lys Leu Trp Leu Lys Lys His Arg Arg Thr Pro
 85 90 95
 Gln Glu Gln Leu Phe Lys Met Leu Pro Asp Thr Phe Pro His Pro His
 100 105 110
 Glu Thr Thr Gly Asp Ala Gln Cys Ser Gln Asn Glu Asn Asp Glu Asp
 115 120 125
 Ser Asp Gly Glu Glu Thr Lys Val Gln His Thr Ala Leu Leu Leu Pro
 130 135 140
 Val Glu Thr Leu Asn Ile Glu Arg Pro Glu Pro Ser Leu Lys Ile Val
 145 150 155 160
 Glu Leu Asp Asp Thr Tyr Glu Glu Glu Phe Glu Glu Ala Glu Asn Ile
 165 170 175
 Val Pro Tyr Lys Val Lys Leu Ala Asp Ala Asp Ser Gln Arg Ser Cys

180	185	190
Ala Phe His Asp Cys Gln Lys Asn Ser Phe Pro Tyr Glu Asn Gly Ile 195 200 205		
His Gln His His Val Phe Asp Lys Gly Lys Arg Asp Phe Leu Asn Leu 210 215 220		
Cys Leu Arg Asn Ser Tyr Thr Tyr Tyr Lys Asp Asn Ser Lys Ala Glu 225 230 235 240		
Thr Ser Asn Thr Asp Phe Asp Asn Ile Val Asp Pro Asp Val Tyr Ser 245 250 255		
Ser Asp Ile Glu Lys Ile Glu Glu Ser Thr Ser Phe Glu Arg Asn Leu 260 265 270		
Lys Glu Lys Asn Ile Gly Leu Glu Ser Asn Gln Lys Ser Asp Asp Ser 275 280 285		
Cys Val Ser Leu Glu Ser Lys Asp Thr Leu Leu Gly Arg Asp Leu Glu 290 295 300		
Lys Ala Pro Ile Glu Glu Lys Leu Ser Gln Asp Ile Lys Glu Ser Leu 305 310 315 320		
Glu Leu Ser Asn Leu Tyr Lys Arg Pro Ser Phe Glu Glu Ser Lys Thr 325 330 335		
Thr Lys Ser Ser Leu Leu Leu Gln Glu Ile Ala Cys Arg Ser Lys Pro 340 345 350		
Ile Thr Lys Gln Tyr Gln Gly Leu Glu Arg Phe Phe Ile Phe Asp Thr 355 360 365		
Asn Glu Arg Leu Asn Leu Leu Pro Ser His Arg Leu Glu Cys Asn Asn 370 375 380		
Ser Ser Thr Arg Ile Thr Leu Ala Glu Asp Arg Glu Trp Ile Pro Asp 385 390 395 400		
His Ser Leu Ser Glu Tyr Ala Asp Asn Ala Ile Val Leu Gly Val Leu 405 410 415		
Gln Gly Ala Gln Ser Pro Ser Ser Ser Arg Lys Gln Gln Lys Met Gly 420 425 430		
Gln Lys Ser Gln Arg Pro Ser Thr Ala Asn Phe Pro Leu Ser Asn Ser 435 440 445		
Val Lys Glu Ser Ser Ser Cys Leu Ser Ser Ser His Pro Arg Ser Arg 450 455 460		
Ser Ala Ala Ala Gln Ser Ser Ser Arg Ala Ala Ser Glu Ile Ser Glu 465 470 475 480		
Ile Glu Tyr Ile Asp Ile Thr Asp Gln Asn Glu Leu Ser Leu Asp Asp 485 490 495		
Thr Thr Asp Gln His Thr Leu Asp Asn Leu Glu Lys Glu Leu Gln Val 500 505 510		

Leu Arg Ser Leu Ala Asp Thr Ser Glu Lys Leu Tyr Ser Leu Thr Ser
 515 520 525

Glu Glu Phe Pro Asp Phe Ser Ser Gln Ser Leu Asn Ile Ser Gln Ile
 530 535 540

Ser Thr Asp Phe Leu Lys Thr Ser His Val Arg Gly Pro Cys Gly Val
 545 550 555 560

Glu Glu Leu Ser Cys Ser Gly Arg Asp Thr Lys Ile Gln Ser Leu Leu
 565 570 575

Ser Leu Ser Glu Ser Ser Thr Asp Glu Glu Glu Glu Asp Phe Leu Asn
 580 585 590

Lys Gln His Val Ile Thr Leu Pro Trp Ser Lys Ser Thr
 595 600 605

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GTCCTGGATG	GCGGAGCCTT	GGGTTCCGGG	GGCCTGGGAC	CTGCAACTCT	TTCTACAAGA	60
TATCAAGTTA	TTCTAGTACA	ACCATATAAA	TAAATAATAC	CTGAAGTCTC	AGTGTAACAT	120
GGACAATTAA	CAGTGATGAC	AGATAAATAC	AGACGCATGG	GGATCAAATA	CTAGGCCAAA	180
CGCTTTTAA	AAGTGATCA	GGCTTTTAA	AAACACTGCA	GGATCCTGTC	TATCTTAATG	240
CTGATAGAGC	TCAGCTAAAA	ATTTAGGAGG	TTCTAGTATT	CTTCATGGCT	GAAGCTGAGA	300
GAGTCTGAAA	CCCTGATGCT	TAAGCTCCAT	TCTAGATCAT	AGCTCCAAC	CCTTCAGGAT	360
ATAAGGAAAA	GAGATTATAT	TTCCACAATG	ATAGATCTTT	GGTTGTACAG	GTTTCCCAAT	420
GAGTGGATCA	TGATGACCGT	ATTGTAGGGA	CTTGCCATAG	TATGGCTGCT	TCCCGATCTA	480
CTCGTGTTAC	MAGATCAACA	GTGGGGTTAA	ACGGCTTGGA	TGAATCTTTT	TGTGGTAGAA	540
CTTTAAGGAA	TCGTAGCATT	GCGCATCCTG	AAGAAATCTC	TTCTAATTCT	CAAGTACGAT	600
CAAGATCACC	AAAGAAGAGA	CCAGAGCCTG	TGCCAATTCA	GAAAGGAAAT	AATAATGGGA	660
GAACCACTGA	TTTAAACAG	CAGAGTACCC	GAGAATCATG	GGTAAGCCCT	AGGAAAAGAG	720
GACTTTCTTC	TTCAGAAAAG	GATAACATAG	AAAGGCAGGC	TATAGAAAAT	TGTGAGAGAA	780
GGCAAACAGA	ACCTGTTTCA	CCAGTTTTAA	AAAGAATTAA	GCGTTGTCTT	AGATCTGAAG	840
CACCAAACAG	TTCAGAAGAA	GATTCTCCTA	TAAAATCAGA	CAAGGAGTCA	GTAGAACAGA	900
GGAGTACAGT	AGTGGACAAT	GATGCAGATT	TTCAAGGGAC	TAAACGAGCT	TGTCGATGTC	960
TTTACTGGA	TGATTGTGAG	AAAAGGGAAA	TTAAAAGGT	GAATGTCAGT	GAGGAAGGGC	1020
CACTTAATTC	TGCAGTAGTT	GAAGAAATCA	CAGGCTATTT	GGCTGTCAAT	GGTGTGATG	1080
ACAGTGATTG	AGCTGTTATA	AACTGTGATG	ACTGTCAGCC	TGATGGGAAC	ACTAAACAAA	1140
ATAGCATTTG	TTCTATGTG	TTACAGGAAA	AATCAGTAGC	TGAAAATGGG	GATACGGATA	1200
CCCAAACCTT	AATGTTCTT	GATAGTAGGA	AGGAGGACAG	TTATATAGAC	CATAAGGTGC	1260
CTTGACACAGA	TTCACAAGTG	CAGGTCAAGT	TGGAGGACCA	CAAAATAGTA	ACTGCCTGCT	1320
TGCCTGTGGA	ACATGTTAAT	CAGCTGACTA	CTGAGCCAGC	TACAGGGCCC	TTTTCTGAAA	1380
CTCAGTCATC	TTTAAGGGAT	TCTGAGGAGG	AAGTAGATGT	GGTGGGAGAT	AGCAGTGCCT	1440
CAAAAGAGCA	GTGTAAGAA	AACACCAATA	ACGAAGTGA	CACAAGTCTT	GAGAGTATGC	1500
CAGCCTCCGG	AGAACCTGAA	CCATCTCCTG	TTCTAGACTG	TGTATCAGCT	CAAATGATGT	1560
CTTTATCAGA	ACCTCAAGAA	CATCGTTATA	CTCTGAGAAC	CTCACCACGA	AGGGCAGCCC	1620
CTACCAGAGG	TAGTCCCCT	AAAAACAGTT	CTCCTTACAG	AGAAAATGGA	CAATTTGAGG	1680
AGAATAATCT	TAGTCCTAAT	GAAACAAATG	CAACTGTTAG	TGATAATGTA	AGTCAATCTC	1740
CTACAAATCC	TGGTGAAATT	TCTCAAATG	AAAAAGGGAT	ATGTTGTGAC	TCTCAAATA	1800

ATGGAAGTGA AGGAGTAAGT AAACCACCCCT CAGAGGCAAG ACTCAATATT GGACATTTGC 1860
 CATCTGCCAA AGAGAGTGCC AGTCAGCACA TTACAGAAGA GGAAGATGAT GATCCTGATG 1920
 TTTATTACTT TGAATCAGAT CATGTGGCAC TGAACACAAA CAAAGATTAT CAGAGACTAT 1980
 TACAGACGAT TGCTGTACTC GAGGCTCAGC GTTCTCAAGC AGTCCAAGAC CTTGAAAGTT 2040
 TAGGCAGGCA CCAGACGAGA GCACTGAAAA ATCCCATTGG ATTTGTGGAA AAACCTCAGA 2100
 AGAAGGCTGA TATTGGGCTT CCATATCCAC AGAGAGTTGT TCAATTGCCT GAGATCGTAT 2160
 GGGACCAATA TACCCATAGC CTTGGGAATT TTGAAAGAGA ATTTAAAAAT CGTAAAAGAC 2220
 ATACTAGAAG AGTTAAGCTA GTTTTTGATA AAGTAGGTTT ACCTGCTAGA CAAAAAGTC 2280
 CTTTAGATCC TAAGAAGGAT GGAGAGTCCC TTTCATATTC TATGTTGCCT TTGAGTGATG 2340
 GTCCAGAAGG CTCAAGCAGT CGTCCTCAGA TGATAAGAGG ACGCTTGTGT GATGATACCA 2400
 AACCTGAAAC ATTTAACCAG TTGTGGACTG TTGAAGAACA GAAAAAGCTG GAACAGCTAC 2460
 TCATCAAAATA CCCTCCTGAA GAAGTAGAAT CTCGACGCTG GCAGAAGATA GCAGATGAAT 2520
 TGGGCAACAG GACAGCAAAA CAGGTTGCCA GCCGAGTACA GAAGTATTTT ATAAAGCTAA 2580
 CTAAAGCTGG CATTCCAGTA CCAGGCAGAA CACCAAACCT ATATATATAC TCCAAAAAGT 2640
 CTTCAACAAG CAGACGACAG CACCCTCTTA ATAAGCATCT CTTAAGCCT TCCACTTTCA 2700
 TGACTTCACA TGAACGCCCA GTGTATATGG ATGAAGATGA TGACCGATCT TGTTCATATA 2760
 GCCACATGAA CACTGCTGTT GAAGATGCAT CAGATGACGA AAGTATTCCT ATCATGTATA 2820
 GGAATTTACC TGAATATAAA GAACATTAC AGTTTAAAAA GTTAAAGAAG CAGAACTTC 2880
 AGCAAATGCA AGCTGAAAGT GGATTTGTGC AACATGTGGG CTTAAGTGT GATAACTGTG 2940
 GCATAGAACC CATCCAGGGT GTTCGGTGGC ATTGCCAGGA TTGTCCTCCA GAAATGTCTT 3000
 TGGATTTCTG TGATTCCTGT TCAGACTGTC TACATGAAAC AGATATTCAC AAGGAAGATC 3060
 ACCAATTAGA ACCTATTTAT AGGTCAGAGA CATTCTTAGA CAGAGACTAC TGTGTGTCTC 3120
 AGGGCACCAG TTACAATTAC CTTGACCCAA ACTACTTTCC AGCAAAACAGA TGACATGGAA 3180
 GAGAACATCA TTTACTAGTC CTCTTCAACA CATAGCAATG GTATCATTGT TAATTATGTG 3240
 CACAGTTTGG AAAGATTCTC TGCTTTCCCA GAAATGACAC TCACAGCATG AGAGCTTCCT 3300
 GAGTGTTCTC GTCAAGTACA GCTCTGCACC GTTGTGGCTC TAGATCACTG TTCAGCAGCT 3360
 GAACATTCCT GGTGAGCAAA GGTTTCCCTG GTGAATTTTT CACCACTGCG TTTTAGGTGG 3420
 TGATCTTAAA TGGGTGAGAT GGAACGAGAG CACACATTAA AGAGAGAGTA AATTCCAAAG 3480
 GTTTCAAAGA ACTTGGTCAT AAATATGATA ATGAGAAGAC AAAGTATTTA TATTAAAACA 3540
 GTTTAGTAGC CTTCAGTTTT GTGAAAATAG TTTTCAGCAC AGAAACTGAC TTCTTTAGAC 3600
 AAAGTTTTAA CCAATGATGG TGTTTGCTTC TAGGATATAC ACTTTAAAAG AACTCACTGT 3660
 CCCAGTGGTG GTCATFGATG GCCTTTAGTA AATTGGAGCT GCTTAATCAT ATTGATATCT 3720
 AATTTCTTTT AACCACAATG AATTGTCCTT AATTACCAAC AGTGAAGCAC TACAGGAGGC 3780
 AACTGTGGCA TTGCTTCCTT AACCAGCTCA TGGTGTGTGA ATGTTATAAA ATTGTCATC 3840
 AGATATATTT TTTAAATGTA ATGTTATATA AGATGATCAT GTGATGTGTA CAACTATGG 3900
 TGAAAAGTGC CAGTGGTAGT AACTGTGTAA AGTTTCTAAT TCACAACATT AATTCCTTTA 3960
 AAATACACAG CCTTCTGCCT CTGTATTGG AGTTGTCAGT ACAACTCATC AAAGAAAAC 4020
 GCCTAATATA AAAATCATAT ATATGGTAAT AATTTCCCTC TTTTGTAGTC TGCACAAGAT 4080
 CCATAAAAGA TTGTATTTTT ATTACTATTT AAACAAGTGA TTAAATTTAG TCTGCACAGT 4140
 GAGCAAGGGT TCACATGCAT TCTTTTATAC TGCTGGATTT TGTTGTGCAT CATTTAAAAC 4200
 ATTTTGTATG TTTCTCTTA TCTGTGTATA CAGTATGTTT TTGAATGATG TTCATTTGTC 4260
 AGGAGAACTG TGAGAAATAA ACTATGTGGA TACTGTCTGT TTMTRTCAAA AAAAAAAAAA 4320
 AAAAAAAAAA AAAAAAA 4337

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Ala Ala Ser Arg Ser Thr Arg Val Thr Arg Ser Thr Val Gly Leu
 1 5 10 15

Asn Gly Leu Asp Glu Ser Phe Cys Gly Arg Thr Leu Arg Asn Arg Ser
 20 25 30

Ile Ala His Pro Glu Glu Ile Ser Ser Asn Ser Gln Val Arg Ser Arg
35 40 45

Ser Pro Lys Lys Arg Pro Glu Pro Val Pro Ile Gln Lys Gly Asn Asn
50 55 60

Asn Gly Arg Thr Thr Asp Leu Lys Gln Gln Ser Thr Arg Glu Ser Trp
65 70 75 80

Val Ser Pro Arg Lys Arg Gly Leu Ser Ser Ser Glu Lys Asp Asn Ile
85 90 95

Glu Arg Gln Ala Ile Glu Asn Cys Glu Arg Arg Gln Thr Glu Pro Val
100 105 110

Ser Pro Val Leu Lys Arg Ile Lys Arg Cys Leu Arg Ser Glu Ala Pro
115 120 125

Asn Ser Ser Glu Glu Asp Ser Pro Ile Lys Ser Asp Lys Glu Ser Val
130 135 140

Glu Gln Arg Ser Thr Val Val Asp Asn Asp Ala Asp Phe Gln Gly Thr
145 150 155 160

Lys Arg Ala Cys Arg Cys Leu Ile Leu Asp Asp Cys Glu Lys Arg Glu
165 170 175

Ile Lys Lys Val Asn Val Ser Glu Glu Gly Pro Leu Asn Ser Ala Val
180 185 190

Val Glu Glu Ile Thr Gly Tyr Leu Ala Val Asn Gly Val Asp Asp Ser
195 200 205

Asp Ser Ala Val Ile Asn Cys Asp Asp Cys Gln Pro Asp Gly Asn Thr
210 215 220

Lys Gln Asn Ser Ile Gly Ser Tyr Val Leu Gln Glu Lys Ser Val Ala
225 230 235 240

Glu Asn Gly Asp Thr Asp Thr Gln Thr Ser Met Phe Leu Asp Ser Arg
245 250 255

Lys Glu Asp Ser Tyr Ile Asp His Lys Val Pro Cys Thr Asp Ser Gln
260 265 270

Val Gln Val Lys Leu Glu Asp His Lys Ile Val Thr Ala Cys Leu Pro
275 280 285

Val Glu His Val Asn Gln Leu Thr Thr Glu Pro Ala Thr Gly Pro Phe
290 295 300

Ser Glu Thr Gln Ser Ser Leu Arg Asp Ser Glu Glu Glu Val Asp Val
305 310 315 320

Val Gly Asp Ser Ser Ala Ser Lys Glu Gln Cys Lys Glu Asn Thr Asn
325 330 335

Asn Glu Leu Asp Thr Ser Leu Glu Ser Met Pro Ala Ser Gly Glu Pro
340 345 350

Glu Pro Ser Pro Val Leu Asp Cys Val Ser Ala Gln Met Met Ser Leu
 355 360 365
 Ser Glu Pro Gln Glu His Arg Tyr Thr Leu Arg Thr Ser Pro Arg Arg
 370 375 380
 Ala Ala Pro Thr Arg Gly Ser Pro Thr Lys Asn Ser Ser Pro Tyr Arg
 385 390 395 400
 Glu Asn Gly Gln Phe Glu Glu Asn Asn Leu Ser Pro Asn Glu Thr Asn
 405 410 415
 Ala Thr Val Ser Asp Asn Val Ser Gln Ser Pro Thr Asn Pro Gly Glu
 420 425 430
 Ile Ser Gln Asn Glu Lys Gly Ile Cys Cys Asp Ser Gln Asn Asn Gly
 435 440 445
 Ser Glu Gly Val Ser Lys Pro Pro Ser Glu Ala Arg Leu Asn Ile Gly
 450 455 460
 His Leu Pro Ser Ala Lys Glu Ser Ala Ser Gln His Ile Thr Glu Glu
 465 470 475 480
 Glu Asp Asp Asp Pro Asp Val Tyr Tyr Phe Glu Ser Asp His Val Ala
 485 490 495
 Leu Lys His Asn Lys Asp Tyr Gln Arg Leu Leu Gln Thr Ile Ala Val
 500 505 510
 Leu Glu Ala Gln Arg Ser Gln Ala Val Gln Asp Leu Glu Ser Leu Gly
 515 520 525
 Arg His Gln Arg Glu Ala Leu Lys Asn Pro Ile Gly Phe Val Glu Lys
 530 535 540
 Leu Gln Lys Lys Ala Asp Ile Gly Leu Pro Tyr Pro Gln Arg Val Val
 545 550 555 560
 Gln Leu Pro Glu Ile Val Trp Asp Gln Tyr Thr His Ser Leu Gly Asn
 565 570 575
 Phe Glu Arg Glu Phe Lys Asn Arg Lys Arg His Thr Arg Arg Val Lys
 580 585 590
 Leu Val Phe Asp Lys Val Gly Leu Pro Ala Arg Pro Lys Ser Pro Leu
 595 600 605
 Asp Pro Lys Lys Asp Gly Glu Ser Leu Ser Tyr Ser Met Leu Pro Leu
 610 615 620
 Ser Asp Gly Pro Glu Gly Ser Ser Ser Arg Pro Gln Met Ile Arg Gly
 625 630 635 640
 Arg Leu Cys Asp Asp Thr Lys Pro Glu Thr Phe Asn Gln Leu Trp Thr
 645 650 655
 Val Glu Glu Gln Lys Lys Leu Glu Gln Leu Leu Ile Lys Tyr Pro Pro
 660 665 670
 Glu Glu Val Glu Ser Arg Arg Trp Gln Lys Ile Ala Asp Glu Leu Gly

675	680	685
Asn Arg Thr Ala Lys Gln Val Ala Ser Arg Val Gln Lys Tyr Phe Ile 690 695 700		
Lys Leu Thr Lys Ala Gly Ile Pro Val Pro Gly Arg Thr Pro Asn Leu 705 710 715 720		
Tyr Ile Tyr Ser Lys Lys Ser Ser Thr Ser Arg Arg Gln His Pro Leu 725 730 735		
Asn Lys His Leu Phe Lys Pro Ser Thr Phe Met Thr Ser His Glu Pro 740 745 750		
Pro Val Tyr Met Asp Glu Asp Asp Asp Arg Ser Cys Phe His Ser His 755 760 765		
Met Asn Thr Ala Val Glu Asp Ala Ser Asp Asp Glu Ser Ile Pro Ile 770 775 780		
Met Tyr Arg Asn Leu Pro Glu Tyr Lys Glu Leu Leu Gln Phe Lys Lys 785 790 795 800		
Leu Lys Lys Gln Lys Leu Gln Gln Met Gln Ala Glu Ser Gly Phe Val 805 810 815		
Gln His Val Gly Phe Lys Cys Asp Asn Cys Gly Ile Glu Pro Ile Gln 820 825 830		
Gly Val Arg Trp His Cys Gln Asp Cys Pro Pro Glu Met Ser Leu Asp 835 840 845		
Phe Cys Asp Ser Cys Ser Asp Cys Leu His Glu Thr Asp Ile His Lys 850 855 860		
Glu Asp His Gln Leu Glu Pro Ile Tyr Arg Ser Glu Thr Phe Leu Asp 865 870 875 880		
Arg Asp Tyr Cys Val Ser Gln Gly Thr Ser Tyr Asn Tyr Leu Asp Pro 885 890 895		
Asn Tyr Phe Pro Ala Asn Arg 900		

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AATCGGGACC CCATCCCCCA AATCACTGGA TCCTGCAGCC CCACATCCTA AGGTGGATCC 60
 CACGCTTCCC TGTGCCCCCT ACTGGATCCT GGACCTCTAC GTCTTAACCA CTGGATCCCA 120
 CACAAATCAG TGAATGGATC CCAACACCCC AACCACAGGA GCACGGATTC CCTGTACCTC 180
 AACACCCAGA CCCTGCCTCC CTCAGGCACC AGATCCAGTG TCCTAGTGAA ACGCTGGATC 240
 CTAGATCCCC AACCCAGAT CCCCATGCCT CGAGCCCTGG ATCTCCAAGC TCAGCTGCTG 300

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GATTCTGGAT GTCAACAAAC CTCACCACTG GATCCTGACA ACCACAATGC CTGGATCCTG 360
GGGCCCCCAT CACTGGATCC CAGATCCCCT CACTCCACCC ACTGGATTCC TGCATTGGTT 420
TTTGGTTTTT TGTTTTTTTT TTAACCTCGA CACTGGGTCT CAGATCCTTC TGCTGACTGC 480
CAGATCCCTG CATTTCAAGC ACTACGCCTT CCACCCCCAG GCACTGGATC CCAGATTCCC 540
AAGCCTTCAC CCACCAGATT CTGGCTCCTA AAACAAGTGC GGGGGCCCCA GTGGCACAGC 600
AAGTGGATCC TGGCAACTGC AGCTGCTGGA TTCCAGATTG TGGGTCCCCA ATCCCTCTGC 660
CCAGTCCCTC AATGTTGAAA CCTCATCTCT TGAAGGCAGA TCCTGATATT CCAAGGCACT 720
GAATCCCAAG CCCTGAATCC CCGGTTTCTG ATCTGAATCT TCCAGGCGCC GGGTCCCAA 780
TGTTCAAGCC CCAAGTCTAG ATCCTGGCAG CCCAGTCACA GAGTATCCCA CACACACTGG 840
TGCCAGAGC CGGCTTCTCA TGACATGAAA TTGCATGGTC GAGGGAGTCT GTGGGGAAGG 900
AAGCCCAGGT CCTGGCTGCA ACCTGCACGG ATGCTGGATT CCCCTCACC CCACCTCTGC 960
ATGGCCACCC CCTCCCAGCC CTGTGGGGAA ACTGTTCCCT GGAACCACTC CACTCCCTGC 1020
ATCCCCACAC TTCACAGCAT CTTCATCCC CCTCCCCTT CTAGGCGAAT AGTCCCCAGA 1080
GCTGTGTTCC TCCAAGGGGT CCGAGGAATC ACTACTCCT GGAGGCTGGC AAGGAGACAG 1140
TCTGAGGCA GGGACACATG AAGGGATGTC CCCACCCAG CACTATCAGG GCCTCCCCAG 1200
GCTTCCAGAG TTGAAAGCCA GGAGAAATC GGCAAAGACC ACCCTTCCCT AAACCCAAGC 1260
ACCCAATGAT GCRAAAAAA AAAAAAAA AAAAAAAA 1299

```

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

Met Lys Leu His Gly Arg Gly Ser Leu Trp Gly Arg Lys Pro Arg Ser
 1             5             10             15
Trp Leu Gln Pro Ala Arg Met Leu Asp Ser Pro Ser Pro His Leu Cys
          20             25             30
Met Ala Thr Pro Ser Gln Pro Cys Gly Glu Thr Val Pro Trp Asn His
          35             40             45
Ser Thr Pro Cys Ile Pro Thr Leu His Ser Ile Phe His Pro Pro Pro
          50             55             60
Thr Ser Arg Arg Ile Val Pro Arg Ala Val Phe Leu Gln Gly Val Arg
          65             70             75             80
Gly Ile Thr His Ser Trp Arg Leu Ala Arg Arg Gln Ser Glu Ala Arg
          85             90             95
Asp Thr

```

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 791 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

CTCCTCTGTC CACTGCTTTC GTGAAGACAA GATGAAGTTC ACAATTGTCT TTGCTGGACT 60
TCTTGGAGTC TTTCTAGCTC CTGCCCTAGC TAACTATAAT ATCAACGTCA ATGATGACAA 120
CAACAATGCT GGAAGTGGGC AGCAGTCAGT GAGTGTCAAC AATGAACACA ATGTGGCCAA 180
TGTTGACAAT AACACGGAT GGGACTCCTG GAATTCCATC TGGGATTATG GAAATGGCTT 240
TGCTGCAACC AGACTCTTTC AAAAGAAGAC ATGCATTGTG CACAAAATGA ACAAGGAAGT 300
CATGCCCTCC ATTCAATCCC TTGATGCACT GGTCAAGGAA AAGAAGCTTC AGGGTAAGGG 360
ACCAGGAGGA CCACCTCCCA AGGGCCTGAT GTACTCAGTC AACCCAAACA AAGTCGATGA 420
CCTGAGCAAG TTCGGAACAA ACATTGCAAA CATGTGTCGT GGGATTCCAA CATACTGGC 480
TGAGGAGATG CAAGAGGCAA GCCTGTTTTT TTACTCAGGA ACGTGCTACA CGACCAGTGT 540
ACTATGGATT GTGGACATTT CTTTCTGTGG AGACACGGTG GAGAACTAAA CAATTTTTTTA 600
AAGCCACTAT GGATTTAGTC ATCTGAATAT GCTGTGCAGA AAAAATATGG GCTCCAGTGG 660
TTTTTACCAT GTCATTCTGA AATTTTTTCTC TACTAGTTAT GTTTGATTTC TTTAAGTTTC 720
AATAAAATCA TTTAGCCTTG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 780
AAAAAAAAAA A

```

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Met Lys Phe Thr Ile Val Phe Ala Gly Leu Leu Gly Val Phe Leu Ala
 1             5             10             15
Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn Asn Asn
      20             25             30
Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu His Asn Val
      35             40             45
Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp Asn Ser Ile Trp
      50             55             60
Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu Phe Gln Lys Lys Thr
      65             70             75             80
Cys Ile Val His Lys Met Asn Lys Glu Val Met Pro Ser Ile Gln Ser
      85             90             95
Leu Asp Ala Leu Val Lys Glu Lys Lys Leu Gln Gly Lys Gly Pro Gly
      100             105             110
Gly Pro Pro Pro Lys Gly Leu Met Tyr Ser Val Asn Pro Asn Lys Val
      115             120             125
Asp Asp Leu Ser Lys Phe Gly Lys Asn Ile Ala Asn Met Cys Arg Gly
      130             135             140
Ile Pro Thr Tyr Met Ala Glu Glu Met Gln Glu Ala Ser Leu Phe Phe
      145             150             155             160
Tyr Ser Gly Thr Cys Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile
      165             170             175

```


Ser Phe Cys Gly Asp Thr Val Glu Asn
180 185

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2012 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```
CTCAAGTTCA TCATTGTCCT GAGAGAGAGG AGCAGCGCGG TTCTCGGCCG GGACAGCAGA 60
ACGCCAGGGG ACCCTCACCT GGGCGCGCGG GGGCACGGGC TTTGATTGTC CTGGGGTCGC 120
GGAGACCCGC GCGCCTGCCC TGCACGCCGG GCGGCAACCT TTGCAGTCGC GTTGGCTGCT 180
GCGATCGGCC GCGGGGTCCC TGCCGAAGGC TCGGCTGCTT CTGTCCACCT CTTACACTTC 240
TTCATTTATC GGTGGATCAT TTCGAGAGTC CGTCTTGTA ATGTTTGGA CTTTGCTACT 300
TTATTGCTTC TTTCTGGCGA CAGTTCACG ACTCGCCGAG ACCGGCGGAG AAAGGCAGCT 360
GAGCCCGGAG AAGAGCGAAA TATGGGGACC CGGGCTAAAA GCAGACGTCG TCCTTCCCGC 420
CCGCTATTTT TATATTCAGG CAGTGGATAC ATCAGGGAAT AAATTCACAT CTTCTCCAGG 480
CGAAAAGGTC TTCCAGGTGA AAGTCTCAGC ACCAGAGGAG CAATTCAC TA GAGTTGGAGT 540
CCAGGTTTTT GACCGAAAAG ATGGGTCCTT CATAGTAAGA TACAGAATGT ATGCAAGCTA 600
CAAAAATCTG AAGGTGGAAA TTAAATTTCCA AGGGCAACAT GTGGCCAAAT CCCCATATAT 660
TTTAAAAGGG CCGGTTTACC ATGAGAACTG TGA CTGTGCTT CTGCAAGATA GTGCAGCCTG 720
GCTACGGGAG ATGAACTGCC CTGAAACCAT TGCTCAGATT CAGAGAGATC TGGCACATTT 780
CCCTGCTGTG GATCCAGAAA AGATTGCAGT AGAAATCCCA AAAAGATTTG GACAGAGGCA 840
GAGCCTATGT CACTACACCT TAAAGGATAA CAAGGTTTAT ATCAAGACTC ATGGTGAACA 900
TGTAGGTTTT AGAATTTTCA TGGATGCCAT ACTACTTTCT TTGACTAGAA AGGTGAAGAT 960
GCCAGATGTG GAGCTCTTTG TTAATTTGGG AGACTGGCCT TTGGAAAAAA AGAAATCCAA 1020
TTCAAACATC CATCCGATCT TTTCTGGTG TGGCTCCACA GATTCCAAGG ATATCGTGAT 1080
GCCTACGTAC GATTTGACTG ATTCTGTTCT GGAAACCATG GGCCGGGTAA GTCTGGATAT 1140
GATGTCCGTG CAAGCTAACA CGGGTCCTCC CTGGGAAAGC AAAAATTCCA CTGCCGTCTG 1200
GAGAGGGCGA GACAGCCGCA AAGAGAGACT CGAGCTGGTT AAATCAGTA GAAAACACCC 1260
AGAACTCATA GACGCTGCTT TCACCAACTT TTTCTTCTTT AAACAGGATG AAAACCTGTA 1320
TGGTCCCATT GTGAAACATA TTTCATTTTT TGATTTCTTC AAGCATAAGT ATCAAATAAA 1380
TATCGATGGC ACTGTAGCAG CTTATCGCCT GCCATATTTG CTAGTTGGTG ACAGTGTTGT 1440
GCTGAAGCAG GATTCCATCT ACTATGAACA TTTTACAAT GAGCTGCAGC CCTGGAAACA 1500
CTACATTCCA GTTAAGAGCA ACCTGAGCGA TCTGCTAGAA AAACTTAAAT GGGCGAAAGA 1560
TCACGATGAA GAGGCCAAAA AGATAGCAAA AGCAGGACAA GAATTTGCAA GAAATAATCT 1620
CATGGGCGAT GACATATTCT GTTATTATTT CAACTYTTC CAGGAATATG CCAATTTACA 1680
AGTGAGTGAG CCCCAAATCC GAGAGGGCAT GAMAAGGGTA GAACCACAGA CTGAGGACGA 1740
CCTCTTCCST TGTACTTGCC ATAGGAAAAA GACCAAAGAT GAACTSTGAT ATGCAAAATA 1800
ACTTCTATTA GAATAATGGT GCTCTGAAGA CTCTTCTTAA CTAAAAAGAA GAATTTTTTT 1860
AAGTATTAAT TCCATGGACA ATATAAAATC TGTGTGATTG TTTGCAGTAT GAAGACACAT 1920
TTCTACTTAT GCAGTATTCT CATGACTGTA CTTTAAAGTA CATTTT TAGA ATTTTATAAT 1980
AAAACCACCT TTATTTTAAA AAAAAAAAAA AA 2012
```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Phe Gly Thr Leu Leu Leu Tyr Cys Phe Phe Leu Ala Thr Val Pro
1 5 10 15

Ala Leu Ala Glu Thr Gly Gly Glu Arg Gln Leu Ser Pro Glu Lys Ser
20 25 30

Glu Ile Trp Gly Pro Gly Leu Lys Ala Asp Val Val Leu Pro Ala Arg
35 40 45

Tyr Phe Tyr Ile Gln Ala Val Asp Thr Ser Gly Asn Lys Phe Thr Ser
50 55 60

Ser Pro Gly Glu Lys Val Phe Gln Val Lys Val Ser Ala Pro Glu Glu
65 70 75 80

Gln Phe Thr Arg Val Gly Val Gln Val Leu Asp Arg Lys Asp Gly Ser
85 90 95

Phe Ile Val Arg Tyr Arg Met Tyr Ala Ser Tyr Lys Asn Leu Lys Val
100 105 110

Glu Ile Lys Phe Gln Gly Gln His Val Ala Lys Ser Pro Tyr Ile Leu
115 120 125

Lys Gly Pro Val Tyr His Glu Asn Cys Asp Cys Pro Leu Gln Asp Ser
130 135 140

Ala Ala Trp Leu Arg Glu Met Asn Cys Pro Glu Thr Ile Ala Gln Ile
145 150 155 160

Gln Arg Asp Leu Ala His Phe Pro Ala Val Asp Pro Glu Lys Ile Ala
165 170 175

Val Glu Ile Pro Lys Arg Phe Gly Gln Arg Gln Ser Leu Cys His Tyr
180 185 190

Thr Leu Lys Asp Asn Lys Val Tyr Ile Lys Thr His Gly Glu His Val
195 200 205

Gly Phe Arg Ile Phe Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys
210 215 220

Val Lys Met Pro Asp Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro
225 230 235 240

Leu Glu Lys Lys Lys Ser Asn Ser Asn Ile His Pro Ile Phe Ser Trp
245 250 255

Cys Gly Ser Thr Asp Ser Lys Asp Ile Val Met Pro Thr Tyr Asp Leu
260 265 270

Thr Asp Ser Val Leu Glu Thr Met Gly Arg Val Ser Leu Asp Met Met
275 280 285

Ser Val Gln Ala Asn Thr Gly Pro Pro Trp Glu Ser Lys Asn Ser Thr
290 295 300

Ala Val Trp Arg Gly Arg Asp Ser Arg Lys Glu Arg Leu Glu Leu Val
305 310 315 320

Lys Leu Ser Arg Lys His Pro Glu Leu Ile Asp Ala Ala Phe Thr Asn
 325 330 335

Phe Phe Phe Phe Lys Gln Asp Glu Asn Leu Tyr Gly Pro Ile Val Lys
 340 345 350

His Ile Ser Phe Phe Asp Phe Phe Lys His Lys Tyr Gln Ile Asn Ile
 355 360 365

Asp Gly Thr Val Ala Ala Tyr Arg Leu Pro Tyr Leu Leu Val Gly Asp
 370 375 380

Ser Val Val Leu Lys Gln Asp Ser Ile Tyr Tyr Glu His Phe Tyr Asn
 385 390 395 400

Glu Leu Gln Pro Trp Lys His Tyr Ile Pro Val Lys Ser Asn Leu Ser
 405 410 415

Asp Leu Leu Glu Lys Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala
 420 425 430

Lys Lys Ile Ala Lys Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met
 435 440 445

Gly Asp Asp Ile Phe Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala
 450 455 460

Asn Leu Gln Val Ser Glu Pro Gln Ile Arg Glu Gly Met Xaa Arg Val
 465 470 475 480

Glu Pro Gln Thr Glu Asp Asp Leu Phe Xaa Cys Thr Cys His Arg Lys
 485 490 495

Lys Thr Lys Asp Glu Leu
 500

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GNAAGAAGAG AGCAACAGCC AGGACCAAG

29

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

CNCAGGCTAG GCACTGATTC TGCTGGTTC

29

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GNAGACATGA AAGTTGAGCA GAAGGAAAG

29

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GNGGTGCTTT TGATATCCAG CCATCTCTA

29

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CNTGGAAAGA GGAGCAAGAA CCAAGGCAG

29

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TNGGTTTTGT ACGTTGTGCT CTTTTCATC

29

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TNATGGTCTA TATAACTGTC CTCCTTCCT

29

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CNACACTGGG TCTCAGATCC TTCTGCTGA

29

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GNCTCCAAGA AGTCCAGCAA AGACAATTG

29

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ANTGCCAAAC ATTTACAAGA CGGACTCTC

29

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1776 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

AGCTCACAGT AGCCCGGCGG CCCAGGGCAA TCCGACCACA TTTCACCTCTC ACCGCTGTAG 60
GAATCCAGAT GCAGGCCAAG TACAGCAGCA CGAGGGACAT GCTGGATGAT GATGGGGACA 120
CCACCATGAG CCTGCATTCT CAAGCCTCTG CCACAACCTCG GCATCCAGAG CCCC GGCGCA 180
CAGAGCACAG GGCTCCCTCT TCAACGTGGC GACCAGTGGC CCTGACCCTG CTGACTTTGT 240
GCTTGGTGCT GCTGATAGGG CTGGCAGCCC TGGGGCTTTT GTTTTTTCAG TACTACCAGC 300
TCTCCAATAC TGGTCAAGAC ACCATTTCTC AAATGGAAGA AAGATTAGGA AATACGTCCC 360
AAGAGTTGCA ATCTCTTCAA GTCCAGAATA TAAAGCTTGC AGGAAGTCTG CAGCATGTGG 420
CTGAAAAACT CTGTCTGTAG CTGTATAACA AAGCTGGAGC ACACAGGTGC AGCCCTTGTA 480
CAGAACAATG GAAATGGCAT GGAGACAATT GCTACCAGTT CTATAAAGAC AGCAAAAGTT 540
GGGAGGACTG TAAATATTTT TGCCTTAGTG AAAACTCTAC CATGCTGAAG ATAAACAAAC 600
AAGAAGACCT GGAATTTGCC GCGTCTCAGA GCTACTCTGA GTTTTTCTAC TCTTATTGGA 660
CAGGGCTTTT GCGCCCTGAC AGTGGCAAGG CCTGGCTGTG GATGGATGGA ACCCCTTTCA 720
CTTCTGAAGT GTTCCATATT ATAATAGATG TCACCAGCCC AAGAAGCAGA GACTGTGTGG 780
CCATCCTTAA TGGGATGATC TTCTCAAAGG ACTGCAAAGA ATTGAAGCGT TGTGTCTGTG 840
AGAGAAGGGC AGGAATGGTG AAGCCAGAGA GCCTCCATGT CCCCCCTGAA ACATTAGGCG 900
AAGGTGACTG ATTCGCCCTC TGCAACTACA AATAGCAGAG TGAGCCAGGC GGTGCCAAAG 960
CAAGGGCTAG TTGAGACATT GGGAAATGGA ACATAATCAG GAAAGACTAT CTCTCTGACT 1020
AGTACAAAAT GGGTTCTCGT GTTTCCTGTT CAGGATCACC AGCATTCTCTG AGCTTGGGTT 1080
TATGCACGTA TTTAACAGTC ACAAGAAGTC TTATTTACAT GCCACCAACC AACCTCAGAA 1140
ACCCATAATG TCATCTGCCT TCTTGCTTA GAGATAACTT TTAGCTCTCT TTCTTCTCAA 1200
TGTCTAATAT CACCTCCCTG TTTTCATGTC TTCCTTACAC TTGGTGGAAT AAGAACTTTT 1260
TTGAAGTAGA GGAAATACAT TGAGGTAACA TCCTTTTCTC TGACAGTCAA GTAGTCCATC 1320
AGAAATTGGC AGTCACTTCC CAGATTGTAC CAGCAAATAC ACAAGGAATT CTTTTTGT 1380
GTTTCAGTTC ATACTAGTCC CTTCCCAATC CATCAGTAAA GACCCCATCT GCCTTGTC 1440
TGCCGTTTCC CAACAGGGAT GTCACCTGAT ATGAGAATCT CAAATCTCAA TGCCCTTATA 1500
GCATTCCTTC CTGTGTCCAT TAAGACTCTG ATAATTGTCT CCCCTCCATA GGAATTTCTC 1560
CCAGGAAAGA AATATATCCC CATCTCCGTT TCATATCAGA ACTACCGTCC CCGATATTCC 1620
CTTCAGAGAG ATTAAAGACC AGAAAAAAGT GAGCCTCTTC ATCTGCACCT GTAATAGTTT 1680
CAGTTCCTAT TTTCTTCCAT TGACCCATAT TTATACCTTT CAGGTACTGA AGATTTAATA 1740
ATAATAAATG TAAATACTGT GAAAAAATAA AAAAAA 1776

```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly
 1              5              10              15
Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
          20              25              30
Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
          35              40              45
Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
          50              55              60

```

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn
65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys
115 120 125

Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His
130 135 140

Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp
145 150 155 160

Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn
165 170 175

Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe
180 185 190

Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala
195 200 205

Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile
210 215 220

Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
225 230 235 240

Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val
245 250 255

Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro
260 265 270

Pro Glu Thr Leu Gly Glu Gly Asp
275 280

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CAACTATCCC ATAATTTATT TATTCTTCTT CAATGTTTGT AAAGTGCATG AGTCATGTTC 60
ACACTTGAAG TCTAGTAGTG CACTGTAATA ATTCATTTTT TAAAAGATTA TTTAATGCCC 120
ATTTCAAAAT ACAGTAGTTT ACACAGCTAC AGAAACAATT TGGGGCAAGT TTTAAACAC 180
TGAAACAGTA ATAGTTATTG GTGTCACATA AACTGATTT GTTTTTTACA GCCAAACCTC 240
TGTCAGTCAG AGGCATTCAT TAGTTTTATA CATGTAATTT GAAAATCACT AAACCTCGTT 300

```

TTCTCAGCAG CAATAATTTA AGAGGCTTCA AAAATATAAT TTCACTCTTA TTTAGTATTT 360
TTTCCTGGGG GGATTTTTTAC GTAATTTTTT TATGAAAAGA CAAATGCATG TTGAGATAAC 420
TTCTGGGATT AAAATAGTCT TTTGCTTTAC TTTTTTGGTT TCCTAAAACA ACTTTATTGA 480
CTTTTAGTCC ATACTGTTAT ATTTTGTCT TAAAGAAAAT TTAAACTACA AATACCAAAA 540
GAAAACATTT TAAATTTAGG GATGAGACTT TGGGTGATCG TGGGTCTAGG TTTAATGAAC 600
ACATCTGGGG TTAAGTTGGC ATTTCTTCAC ATCTCCACAC CCACACCAAC CATCACAGCC 660
CCCCACCAAC CTTCTCCCAA CCCCAAAAGC ATTGTCCAGG GATATAGATT TTACCAAAGG 720
CTTCCTGGGA AGACGAGGGA GCAACACTTT AGATTAAATG TGATCAGACT TTCCTATTAG 780
ATATGGCTCT TCTGTCTCTT GTTATCCCCC TGACAGCTCT GCCATAAAGT CCCTTCTCCT 840
CATCCTTCCC AAACAGGCTG TATAAGTGCT TTGAGGTAAT TAAACTCTTT CCTCCAGTTT 900
ACAAATATCA CTTACAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA 947

```

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

Met Arg Leu Trp Cys Ile Val Gly Leu Gly Leu Met Asn Thr Ser Gly
 1             5             10             15
Val Lys Leu Ala Phe Leu His Ile Ser Thr Pro Thr Pro Thr Ile Thr
          20             25             30
Ala Pro His Gln Pro Ser Pro Asn Pro Lys Ser Ile Val Gln Gly Tyr
          35             40             45
Arg Phe Tyr Gln Arg Leu Pro Gly Lys Thr Arg Glu Gln His Phe Arg
          50             55             60
Leu Asn Val Ile Arg Leu Ser Tyr
65             70

```

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```

CGCTGACTTG GGCAATGGGG CCGGTGGGGT TTGGGGGCGG AAGAGACCCT CGGGGTTGAG 60
AAGTATGTGG TGGCCTTTCG TCCCCTGTAA AACATTGTCA CACGGTGTGG GGCGGCAGCG 120
CTGGATCTTT GCAAGGCTAT TTTGGCATTC TGCTGGATAT ATGTTCTGTA ATACCAAAGT 180
CGGCGGGAAA GTGAAGTTGT CTCCACCATA ACAGCAATTT TTTCTCTAGC AATTGCACTT 240
ATCACATCAG CACTTCTACC AGTGGATATA TTTTGGTTT CTTACATGAA AAATCAAAAT 300
GGTACATTTA AGGACTGGGC TAATGCTAAT GTCAGCAGAC AGATTGAGGA CACTGTATTA 360
TACGGTTACT ATACTTTATA TTCTGTTATA TTGTTCTGTG TGTTCTTCTG GATCCCTTTT 420
GTCTACTTCT ATTATGAAGA AAAGGATGAT GATGATACTA GTAAATGTAC TCAAATTAAA 480
ACGGCACTCA AGTATACTTT GGGATTTGTT GTGATTTGTG CACTGCTTCT TTTAGTTGGT 540

```



```

GCCTTTGTTT CATTGAATGT TCCCAATAAC AAAAATTCTA CAGAGTGGGA AAAAGTGAAG 600
TCCCTATTTG AAGAACTTGG AAGTAGTCAT GGTTTAGCTG CATTGTCATT TTCTATCAGT 660
TCTCTGACCT TGATTGGAAT GTTGGCAGCT ATAACCTACA CAGCCTATGG CATGTCTGCG 720
TTACCTTTAA ATCTGATAAA AGGCACTAGA AGCGCTGCTT ATGAACGTTT GGAAAAACAT 780
GAAGACATTG AAGAAGTAGA ACAACACATT CAAACGATTA AATCAAAAAG CAAAGATGGT 840
CGACCTTTGC CAGCAAGGGA TAAACGCGCC TTAAACAAT TTGAAGAAAAG GTTACGAACA 900
CTTAAGAAGA GAGAGAGGCA TTTAGAATTC ATTGAAAACA GCTGGTGGAC AAAATTTTGT 960
GGCGCTCTGC GTCCCCTGAA GATCGTCTGG GGAATATTTT TCATCTTAGT TGCATTGCTG 1020
TTTGTAATTT CTCTTTTCTT GTCAAATTTA GATAAAGCTC TTCATTGAGC TGGAATAGAT 1080
TCTGGTTTCA TAATTTTTTG AGCTAACCTG AGTAATCCAC TGAATATGCT TTTGCCTTTA 1140
CTACAAACAG TTTTCCCTCT TGATTATATT CTTATAACAA TTATTATTAT GTACTTTATT 1200
TTTACTTCAA TGGCAGGAAT TCGAAATATT GGCATATGGT TCTTTTGGAT TAGATTATAT 1260
AAAATCAGAA GAGGTAGAAC CAGGCCCCAA GCACTCCTTT TTCTCTGCAT GATACTTCTG 1320
CTTATTGTCC TTCACACTAG CTACATGATT TAGAGTCTTG CTCCCAATA TGTATGTAT 1380
GGAAGCCAAA ATTACTTAAT AGAGACTAAT ATAACCTCTG ATAATCATAA AGGCAATTCA 1440
ACCTTTTCTG TGCCAAAGAG ATGTGATGCA GATGCTCCTG AAGATCAGTG TACTGTTACC 1500
CGGACATACC TATTCCTTCA CAAGTTCTGG TTCTTCAGTG CTGCTTACTA TTTTGGTAAC 1560
TGGGCCTTTC TTGGGGTATT TTTGATTGGA TTAATTGTAT CCTGTTGTAA AGGGAAGAAA 1620
TCGGTTATTG AAGGAGTAGA TGAAGATTCA GACATAAGTG ATGATGAGCC CTCTGTCTAT 1680
TCTGCTTGAC AGCCTTCTGT CTTAAAGGTT TTATAATGCT GACTGAATAT CTGTTATGCA 1740
TTTTTAAAGT ATTAACTAA CATTAGGATT TGCTAACTAG CTTTCATCAA AAATGGGAGC 1800
ATGGCTATAA GACAACTATA TTTTATTATA TGTTTCTGA AGTAACATTG TATCATAGAT 1860
TAACATTTTA AATTACCATA ATCATGCTAT GTAAATATAA GACTACTGGC TTTGTGAGGG 1920
AATGTTTGTG CAAAATTTT TCCTCTAATG TATAATAGTG TTAAATTGAT TAAAAATCTT 1980
CCAGAATTAA TATTCCTTT TGTCACTTT TGAAACATA ATAAATCATT TGTATCTGTG 2040
CCTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2100
AAAAAAAAAA AAAAAAAAAA

```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```

Met Lys Asn Gln Asn Gly Thr Phe Lys Asp Trp Ala Asn Ala Asn Val
 1             5             10             15
Ser Arg Gln Ile Glu Asp Thr Val Leu Tyr Gly Tyr Tyr Thr Leu Tyr
          20             25             30
Ser Val Ile Leu Phe Cys Val Phe Phe Trp Ile Pro Phe Val Tyr Phe
          35             40             45
Tyr Tyr Glu Glu Lys Asp Asp Asp Thr Ser Lys Cys Thr Gln Ile
          50             55             60
Lys Thr Ala Leu Lys Tyr Thr Leu Gly Phe Val Val Ile Cys Ala Leu
          65             70             75             80
Leu Leu Leu Val Gly Ala Phe Val Pro Leu Asn Val Pro Asn Asn Lys
          85             90             95
Asn Ser Thr Glu Trp Glu Lys Val Lys Ser Leu Phe Glu Glu Leu Gly
          100            105            110

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Ser Ser His Gly Leu Ala Ala Leu Ser Phe Ser Ile Ser Ser Leu Thr
115 120 125

Leu Ile Gly Met Leu Ala Ala Ile Thr Tyr Thr Ala Tyr Gly Met Ser
130 135 140

Ala Leu Pro Leu Asn Leu Ile Lys Gly Thr Arg Ser Ala Ala Tyr Glu
145 150 155 160

Arg Leu Glu Asn Thr Glu Asp Ile Glu Glu Val Glu Gln His Ile Gln
165 170 175

Thr Ile Lys Ser Lys Ser Lys Asp Gly Arg Pro Leu Pro Ala Arg Asp
180 185 190

Lys Arg Ala Leu Lys Gln Phe Glu Glu Arg Leu Arg Thr Leu Lys Lys
195 200 205

Arg Glu Arg His Leu Glu Phe Ile Glu Asn Ser Trp Trp Thr Lys Phe
210 215 220

Cys Gly Ala Leu Arg Pro Leu Lys Ile Val Trp Gly Ile Phe Phe Ile
225 230 235 240

Leu Val Ala Leu Leu Phe Val Ile Ser Leu Phe Leu Ser Asn Leu Asp
245 250 255

Lys Ala Leu His Ser Ala Gly Ile Asp Ser Gly Phe Ile Ile Phe Gly
260 265 270

Ala Asn Leu Ser Asn Pro Leu Asn Met Leu Leu Pro Leu Leu Gln Thr
275 280 285

Val Phe Pro Leu Asp Tyr Ile Leu Ile Thr Ile Ile Ile Met Tyr Phe
290 295 300

Ile Phe Thr Ser Met Ala Gly Ile Arg Asn Ile Gly Ile Trp Phe Phe
305 310 315 320

Trp Ile Arg Leu Tyr Lys Ile Arg Arg Gly Arg Thr Arg Pro Gln Ala
325 330 335

Leu Leu Phe Leu Cys Met Ile Leu Leu Leu Ile Val Leu His Thr Ser
340 345 350

Tyr Met Ile Tyr Ser Leu Ala Pro Gln Tyr Val Met Tyr Gly Ser Gln
355 360 365

Asn Tyr Leu Ile Glu Thr Asn Ile Thr Ser Asp Asn His Lys Gly Asn
370 375 380

Ser Thr Leu Ser Val Pro Lys Arg Cys Asp Ala Asp Ala Pro Glu Asp
385 390 395 400

Gln Cys Thr Val Thr Arg Thr Tyr Leu Phe Leu His Lys Phe Trp Phe
405 410 415

Phe Ser Ala Ala Tyr Tyr Phe Gly Asn Trp Ala Phe Leu Gly Val Phe
420 425 430

Leu Ile Gly Leu Ile Val Ser Cys Cys Lys Gly Lys Lys Ser Val Ile

435

440

445

Glu Gly Val Asp Glu Asp Ser Asp Ile Ser Asp Asp Glu Pro Ser Val
 450 455 460

Tyr Ser Ala
 465

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```

GTTCCGAAAT AAAAGATTTT GCAAACCACT TTCCTACGTA CGTCCACTGT AGTTTTTGCA 60
GATACAACAC TAGCTGTAGC AAAGCCTATG TAAATCATAT GATGAGCTTT CATAGTAACC 120
GTCCAAGCAA AAGGTTTTGT ATTTTAAAGA AGCATTCAGA AAATCTCCGG GGCATTACTC 180
TAGTGTGCCT TAATTGTGAT TTCCTAAGTG ATGTTTCTGG CTTAGATAAT ATGGCTACAC 240
ACTTAAGTCA ACATAAAACT CATACTTGCC AAGTTGTAAT GCAGAAAGTT TCTGTTTGTA 300
TCCCAACTTC TGAGCACCTT TCTGAATTAA AAAAAGAAGC TCCCGCAAAG GAACAAGAAC 360
CTGTGTCTAA GGAAATTGCA AGACCTAACA TGGCTGAAAG AGAAACAGAA ACATCAAATT 420
CTGAAAGTAA ACAAGATAAA GCTGCTTCTT CAAAAGAAAA AAATGGATGT AATGCAAATT 480
CATTTGAAGG CTCATCAACA ACAAAAAGTG AAGAAAGCAT AACAGTTTCA GATAAGGAAA 540
ATGAAACAGG TCTTGACAGC CAGGAACTG GCTCAAAAAA CATCGTCAGT TGTGATTCAA 600
ATATTGGTGC AGATAAAGTG GAAAAGAAAA AACAAATACA ACACGTTTGT CAGGAAATGG 660
AGTTGAAGAT GTGCCAAAGT TCAGAAAACA TAATCTTATC TGATCAGATT AAAGATCACA 720
ACTCCAGTGA AGCCAGATT TCTTCAAAGA ATATTAAGGA TTTGCGATTA GCATCAGATA 780
ATGTAAGCAT TGATCAGTTT TTGAGAAAAA GACATGAACC TGAATCTGTT AGTTCTGATG 840
TTAGCGAGCA AGGCAGTATT CATTTGGAAC CTCTGACTCC ATCCGAGGTA CTTGAGTATG 900
AAGCCACAGA GATTCTTCAG AAAGGTAGTG GTGATCCTTC AGCCAAGACT GATGAAGTAG 960
TGTCTGATCA AACAGATGAC ATTCTGGAG GAAATAACCC TAGCACAACA GAGGCAACAG 1020
TAGACCTGGA AGATGAAAAA GAAAGAAGTT GAAATTAGTC ATTTTAAGTT TCAGTGTACC 1080
AACGATAAGG GCAATTGGAA CAGTGCTATC AGGTGAGCTC AGTGGTGCTG TTGTAGGTTT 1140
AGAAATGGAA ATATGTAAGG GAGGTCACAC ATACACTTTA CCTGTATGTT CAACCTATG 1200
TATCAAACAA ATCAATTCAC CAATAATAGC ATGATTAGTA GGGATTCCCA AAAAGTTTTT 1260
AAAAACACGA ACAGGATTTT AATGATAATT AAATTGTCAG TGGAAGGTC TCATTTAATG 1320
GTTTTCAAGG AAATGGGATT TGGTTGCTGA CATGAATTGA TGATATTAGT AATATTTATA 1380
AAGCCTTTCA AACTTCCATC AATCCTAAGC TAAAAATCTT TATTACCTGT ATATCCTTTT 1440
CAGTTAACTG AGAGGAAGGG ATTTGGAAAC CATGTACTTT TGGGGAGTAA TTGATTAAAA 1500
ACAATGGCTG ATTGGCATTG TTAATGAAGG CTTTATTTGT GAGGATGATG CTGGTAAATG 1560
GAGCATGCTT AGAGTACTAA ATTGATCTAA TGAGAATTTG GATGAACATA AACTTAATTT 1620
TGGATTTAAT ATAACATTCC AGTCAGACGC ATGTAAACAG AATATTTGAA TCTTTGTACC 1680
TCCATACAAG TGTTAGCCTG CCAGGCTGTA AGCTTACCTT AATTAACTT TCAGTGAAAG 1740
TGGAATTATT AAGATATAAA TTTATATTTG TGCTTTTTGT CAGTGTGTAA GCTGTGTAGA 1800
AATTCCTTGA TGTATTAGTT GTATTAATGT AAAGTAGAAA CCCATTGTTG AAACCTCTGT 1860
AGCTATTATG CTTTAAATAT TGTTTAATG ATCTTCCTTA GAAATAGGCC CATAAAAATG 1920
GTCTGGAAGC CAAACCAAAG TATGGTATAA TGATGATATT GTAAAGCAGT AAACGTAAAA 1980
CATGTCCTGG CATGTATTCA GCCATGTTTA AGTGACTTTT CTGTAATTGT AAAATAAAAA 2040
CTTCAAATGG GACCTAAAC AGTGATGTAA AAGAACTGGT TTTGGAAATT TAGCCTAATT 2100
TATCTATAAG ATGGCTGCTA AATTGATTTT TCAGTTCTTT TTATCATCTA GAATATAATA 2160
GATATAGAAA TGAATAATAT GAAGAACAGT AGTTTGCTTT GAAATACTAA TAACTTTTAA 2220
TTTAAATGCT TTCATTTTAA CTTCTTAAAA TGTGCTTTGG ATTCTTAAAT TTTGTTTAC 2280
TGAATGTTCA ATGTTTTTAA TGGCGATTAA AATACTCTGC TGTATATAGT AGTTTTTGAG 2340

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TAAATATTTG CAATAAAAAT CTGCCCCCGA ATAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2400
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAAAAAA AAAAAAAAAA AAAAAA 2487

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met Met Ser Phe His Ser Asn Arg Pro Ser Lys Arg Phe Cys Ile Phe
 1 5 10 15
 Lys Lys His Ser Glu Asn Leu Arg Gly Ile Thr Leu Val Cys Leu Asn
 20 25 30
 Cys Asp Phe Leu Ser Asp Val Ser Gly Leu Asp Asn Met Ala Thr His
 35 40 45
 Leu Ser Gln His Lys Thr His Thr Cys Gln Val Val Met Gln Lys Val
 50 55 60
 Ser Val Cys Ile Pro Thr Ser Glu His Leu Ser Glu Leu Lys Lys Glu
 65 70 75 80
 Ala Pro Ala Lys Glu Gln Glu Pro Val Ser Lys Glu Ile Ala Arg Pro
 85 90 95
 Asn Met Ala Glu Arg Glu Thr Glu Thr Ser Asn Ser Glu Ser Lys Gln
 100 105 110
 Asp Lys Ala Ala Ser Ser Lys Glu Lys Asn Gly Cys Asn Ala Asn Ser
 115 120 125
 Phe Glu Gly Ser Ser Thr Thr Lys Ser Glu Glu Ser Ile Thr Val Ser
 130 135 140
 Asp Lys Glu Asn Glu Thr Cys Leu Ala Asp Gln Glu Thr Gly Ser Lys
 145 150 155 160
 Asn Ile Val Ser Cys Asp Ser Asn Ile Gly Ala Asp Lys Val Glu Lys
 165 170 175
 Lys Lys Gln Ile Gln His Val Cys Gln Glu Met Glu Leu Lys Met Cys
 180 185 190
 Gln Ser Ser Glu Asn Ile Ile Leu Ser Asp Gln Ile Lys Asp His Asn
 195 200 205
 Ser Ser Glu Ala Arg Phe Ser Ser Lys Asn Ile Lys Asp Leu Arg Leu
 210 215 220
 Ala Ser Asp Asn Val Ser Ile Asp Gln Phe Leu Arg Lys Arg His Glu
 225 230 235 240

Pro Glu Ser Val Ser Ser Asp Val Ser Glu Gln Gly Ser Ile His Leu
245 250 255

Glu Pro Leu Thr Pro Ser Glu Val Leu Glu Tyr Glu Ala Thr Glu Ile
260 265 270

Leu Gln Lys Gly Ser Gly Asp Pro Ser Ala Lys Thr Asp Glu Val Val
275 280 285

Ser Asp Gln Thr Asp Asp Ile Pro Gly Gly Asn Asn Pro Ser Thr Thr
290 295 300

Glu Ala Thr Val Asp Leu Glu Asp Glu Lys Glu Arg Ser
305 310 315

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

TTTATTTTTC AAATCATAAT TTTAAAATGA TAGATACCAT TTTGTGATAA CAACAATTCA 60
GAAAACAATT TTCTATCCTC TTAGTTGAAA GAATGTAGGT ACAGTTTGGA TACTTGTA 120
TTAATTTTAG AGTAAACATC TGCATTATAC TCTTATAGAT AATAGAATTA TTTAGTTAAG 180
AAATTCCTTA CAGTAAATGA GATAATGTGT GAAAAAGTAT TTTGTAAATG CTGAGGATTC 240
TACAAATGAT AGTTGTTATT TTCATGTGTA TTTGTAAGAT CATGTCCATT TCATGAATAT 300
AGGACTTCAC ATAAAAAAG ACTTCTCTCA GACAACCTTA TATTCTAGTA TTTTCTGTT 360
GTAAAAAGTA TTAATATTTT ACTTTTATTT TGTTATACAT TTATTTTAAT ATCCATGTGT 420
TTATTATAGT AAATTTGAAA TGAAATCCTG AAAAACAGAA TTTTTTTTAA CACAGACCTC 480
ACACCAATAT TAATTTTTTC TCTACATAAT TTAAACTAC ATAAATTAAG TACTTAAAAT 540
TTATATTGAA GGCCACCAAG AACTTAGGTT GAATCCTAGA AAATTTAAAT AACTATTTTT 600
AAAGTTACCC AACTTAATAT TTTAATTTTT TAATATTTAT CTTCCCTTAC TAATTCTTGA 660
TAAATAATAG CATTAGACTT GATAAAATAA AAAAGAATTT TAGAGTAGAA TTAATATATC 720
AAAAGGGGTA TATCAACCAA ATTGGTGTCA GATTGTATTC ATTCTCTCAT CACATAAAGA 780
TTTTTCTTTT GATAGGTGAT GCTCATATGA ACCTTTGGTT TAGAATCTAT ATATGTACAT 840
GTGTATGTAT GTAGATAGTA TGGTTGTATA CACACATATA TACCAAACAC CATGAATTTT 900
AGCAGTCTGT GATGATCAGC AAAAAAGCAC ATAAAGTAAA ATTAGTTGAC CATGCTAAAT 960
TCAATTCTGG AATTTTTTTT TATTTGGGCA TTTCTAGAAC TTTTACATT TGAAAGTACA 1020
TGATGAGTAT TAGTAACGAT GACTTATGTA TAATCAGAAT CTTTATGACA ATTTAGTTTT 1080
ACAAGGTCAG AAGAGATGAG TTTGCTAAAC CCAGCTGTGA TACCTCAGTT GGAAAGGGAA 1140
TTCAAAGGTA TGCTTTGTAG AACAGAAAAG TATAGTTTTT TTTTCATGAA CTTAATCAT 1200
TTTCTGTTTT TCCTCTATGT GAGTCAGCTA CAAAAGTGGT CTAATTTTAA CAACAGTAGA 1260
ACTTCCTCCT TTTCTACTGT AATCTTCCCA CTGACTTTAC TGCACAGGTA TGAAATACTA 1320
GTGTATTGGA TCTTCAGTAA CCTTTTATT TCTAGATGA TTGAAATATA GGTATTTACT 1380
CCATTTAAAC CAGGTGATAA GATGATGTAA ATACTCAGGG AGGGTATTAA CTTGTACTT 1440
TTGCTCGTTT GGGGTGTAAA GTGCCATGAC TGAATAATCT TCAATTCTAG ATTCTAGAGT 1500
AAGTTTAATT TGGAAAAGG GGCTTCACAC ATGGTGGTGG TTGAACATTG ATTCTTTTAT 1560
ACTTAAAAAG ATGAAAATGT TTTGTGGACT GATACATTTT ATCTTACTGA ATATGAATTG 1620
TTTATGTATC TCTACTGTCA AATAGCCTTT TTGAACTCA GGAAAGACAA AGGTTCAATT 1680
ACACCACTTT TGTCATAAAG CAAACCAGGT ATTTTTTTTT TCTCCTGTTG TCTGGATATG 1740
GCAATAGATT TTTTAAATTG CTGTGAGAAC CCATATATGA AAAGAGAGGA GTTGAATTGT 1800
GTGTGCCTTT TATGTCTTGA GATTTATATG TGGAAAAGAC GACATCTACT TCAAACGTGA 1860
TTTTTTTCGT TTTTTTTTTT TTTTGGGGA AGGGGGGAGA ACGGGGTCTT GCTCTGTCCG 1920

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CCAGGCTGGA GTGCAGTGGC GCGATCTCAG CTGACTGCAA CCTCCACCTC CCGGGTTCAA 1980
 GGGATTCTGC CTCAGCCTCC CGAGTAGCTG AGACCACAGG TGCGTGCCAC CACACCCGGC 2040
 TAATTTTTTT GTATTTTTAG TAGAGACGGG GTTTAGTAGA GACGGATCAC TCCTGACCAC 2100
 GTGATCCGCC CACCTCGGCC TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCACCCCC 2160
 GGCCTGTATT TTCAGAGAGG AGAGCTTGGT GTTTTTGTGG TGCCAAGTGG TAAGATAATG 2220
 TCTCTTTGAG GCTTCCTATG GACTGCCTTT ATTTTAGTAA ACTCAAGACA CCAGTTAACC 2280
 TCAACAGAGT TTTGGCCTTA TTAGAATTTG TTGTGCATCT TATTGAAAGC CAGGTTTACA 2340
 TCACCTCACC CCATTATTCT TTTTAGTTAA ATAAATTTAC CATGCCAAGT AACCAGAATG 2400
 GAGCAAATTG GTTGATCTTT AAGGCAGTAG GTTTGACTAG CTAGCTATCA TTATTGTCAC 2460
 ATCTAATGCT AGGCACCAGA AACCATTTGA GCCAGGAGTG TGAATGAATA ATTCCCAGAG 2520
 ACACTTTAGA CATTTTTTAA TGTTTTATAT GACATTTTAC ATTTGTGTGA TTGCCTTAGA 2580
 TATTAAATTT TCCTAGTGCT GATAAAAACA GCAACATTCA TAACTTATTT TATATATTGT 2640
 TCCAAAGAAA AGAATTTGTT TTAATGGTTT CAAAATAACT GCACCTGAAT TTGTTTATGT 2700
 GCCTTAAGTT CTCTAGTGCT ATTTCAACTT TTTTTTCAAT CTAAATGAAG CTTACCTTAG 2760
 ATAAGGTTCA TATTTGTTTC CTATAGAGTA AATAAACTTC CCCTTCTTAA ATTGTGTAAT 2820
 AAGCACCAAC GTGTGGTTGC TTGGCAGAAT GAGAATGTTA AGGGAGATTG TTGGATGTTT 2880
 GGAGTTTCAT TATATTTTTT GTTTTTATTT TTTGATACCT AGGTGCTTTT TAAATATTTT 2940
 AGACAAATAT CTATCTTACA TTGATTAAAC CCGTGTAAT TCATTTGCAG TATCTACATC 3000
 GAATGTCAAA AAAGTATACT TATTTTTGTT CCATACTTAT GTACAATTTT TTCCCTCTTC 3060
 AGGCTTTTTT ATTTACCTTT TTGAAAAAGC ACTTACTCTC CCCTTCCCTA TCACCCCTCC 3120
 CCCAAGGTTT CTTTATTTAA ATTTTTATTG AGAGTTGTTG GAGCTCTAAG ACAATACAAA 3180
 TTTAGAGTTG AACAAAAGTA TAATCTGCTT TACAAC TAGT ATAGACCTAA GGTCATTTGC 3240
 TTTCAATTAG AGGCTCCAGA GTCTTCATAG TGGAAAGAAT GCTTTGTATT TAATTGTTCT 3300
 TAGTTAAGTT GTAGCACGTG AATACTTACT TACATGTTTT GTTTAAATAT ACTTCTTGCA 3360
 TAGTTTAATT TTTTAAAAGT TGTATCTAAT AAAATGTCTT TTAACCATTA TTAATTGACT 3420
 ATATGGTTGT ATTAAATTTT GTTTACGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3480
 AAAAAAAAAA AAAAA 3495

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ser Lys Lys Tyr Thr Tyr Phe Cys Ser Ile Leu Met Tyr Asn Phe
 1 5 10 15
 Phe Pro Leu Gln Ala Phe Ser Phe Thr Phe Leu Lys Lys His Leu Leu
 20 25 30
 Ser Pro Ser Leu Ser Pro Leu Pro Gln Gly Phe Phe Ile
 35 40 45

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

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GTTGATCCAT CTGAGAAAGG GATCATGAAC TAGACAGAAT GAACAGCCTT AGAGGCACAG 60
ACTCTTGAAC GGGACGGTGG TGGTATGACT AGTGCAGAGT GTTTAGAGAT CACTCAGTTT 120
TTAAAGACTG GCCTTTATCG TGTCTCAGTG CAGCCGAGGC AGAGCCTTTG AAGGATGCGA 180
TGTTGTCATT CTTACTAATC TAGTCCAGCC GCTGAGGTGA CTTTCAACGG CAGACCGTCT 240
CCTGAGCGCC CCAGGTAGAA TTTCAAAGT CTCCGGGACC ATTATGGCAG TCAAGTGGAC 300
GGGTGGGCAT TCTTCTCCTG TCCTCTGCCT GAATGCAAGT AAAGAAGGGC TGCTGGCTTC 360
TGGAGCAGAG GGGCGGAGATC TCACGGCTTG GGGTGAAGAT GGAAGTCCAT TAGGACACAC 420
GCGGTTCCAA GGGGCTGATG ATGTTACCAG TGTCTTATTT TCTCCCTCCT GTCCCACCAA 480
GCTCTATGCC TCACATGGAG AAACCATTAG TGTACTGGAT GTCAGGTCCC TCAAAGATTC 540
CTTGACCAT TTTTCATGTA ATGAAGAAGA AATCAATTGT CTTTCATTGA ATCAAACGGA 600
AAACCTGCTG GCTTCTGCTG ACGACTCTGG GGCAATCAAA ATCCTAGACT TGGAAAACAA 660
GAAAGTTATC AGATCCTTGA AGAGACATTC CAATATCTGC TCCTCAGTGG CTTTTCGGCC 720
TCAGAGGCCT CAGAGCCTGG TGTCATGTGG ACTGGATATG CAGGTGATGC TGTGGAGTCT 780
TCAAAAAGCC CGACCACTCT GGATTACAAA TTTACAGGAG GATGAAACAG AAGAAATGGA 840
AGGCCACAG TCACCTGGTC AGCTCTTAAA CCCTGCCCTA GCCCATTCTA TCTCTGTGGC 900
TTCGTGTGGT AATATTTTTA GTTGTGGTGC AGAAGATGGT AAGGTTTCGAA TCTTTCGGGT 960
GATGGGAGTT AAGTGTGAAC AGGAACTGGG ATTTAAGGGC CACACTTCAG GGGTATCCCA 1020
GGTCTGCTTT CTCCCAGAAT CCTATTTGCT GCTTACTGGA GGAATGATG GGAAGATCAC 1080
GTTGTGGGAT GCAAACAGTG AAGTTGAGAA AAAACAGAAG AGTCCCACAA AACGTACCCA 1140
CAGGAAGAAA CCTAAAAGAG GAACTTGCAC CAAGCAGGGT GGAAATACTA ACGCTTCAGT 1200
AACAGATGAG GAAGAACATG GCAACATTTT ACCGAAGCTA AATATTGAAC ATGGAGAAAA 1260
AGTGAAGTGG CTCTTGGGTA CAAAATATAA GGGACACCAA AATATATTAG TAGCTGATCA 1320
AACTAGTTGT ATATCTGTAT ACCCCTTAAA TGAATTTTAA ATCCAATAAA AACATTTGAA 1380
GAAAAAAAAA AAAAAAAA

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(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

Met Ala Val Lys Trp Thr Gly Gly His Ser Ser Pro Val Leu Cys Leu
 1             5             10             15
Asn Ala Ser Lys Glu Gly Leu Leu Ala Ser Gly Ala Glu Gly Gly Asp
 20            25            30
Leu Thr Ala Trp Gly Glu Asp Gly Thr Pro Leu Gly His Thr Arg Phe
 35            40            45
Gln Gly Ala Asp Asp Val Thr Ser Val Leu Phe Ser Pro Ser Cys Pro
 50            55            60
Thr Lys Leu Tyr Ala Ser His Gly Glu Thr Ile Ser Val Leu Asp Val
 65            70            75            80
Arg Ser Leu Lys Asp Ser Leu Asp His Phe His Val Asn Glu Glu Glu
 85            90            95
Ile Asn Cys Leu Ser Leu Asn Gln Thr Glu Asn Leu Leu Ala Ser Ala
100            105            110

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Asp Asp Ser Gly Ala Ile Lys Ile Leu Asp Leu Glu Asn Lys Lys Val
115 120 125

Ile Arg Ser Leu Lys Arg His Ser Asn Ile Cys Ser Ser Val Ala Phe
130 135 140

Arg Pro Gln Arg Pro Gln Ser Leu Val Ser Cys Gly Leu Asp Met Gln
145 150 155 160

Val Met Leu Trp Ser Leu Gln Lys Ala Arg Pro Leu Trp Ile Thr Asn
165 170 175

Leu Gln Glu Asp Glu Thr Glu Glu Met Glu Gly Pro Gln Ser Pro Gly
180 185 190

Gln Leu Leu Asn Pro Ala Leu Ala His Ser Ile Ser Val Ala Ser Cys
195 200 205

Gly Asn Ile Phe Ser Cys Gly Ala Glu Asp Gly Lys Val Arg Ile Phe
210 215 220

Arg Val Met Gly Val Lys Cys Glu Gln Glu Leu Gly Phe Lys Gly His
225 230 235 240

Thr Ser Gly Val Ser Gln Val Cys Phe Leu Pro Glu Ser Tyr Leu Leu
245 250 255

Leu Thr Gly Gly Asn Asp Gly Lys Ile Thr Leu Trp Asp Ala Asn Ser
260 265 270

Glu Val Glu Lys Lys Gln Lys Ser Pro Thr Lys Arg Thr His Arg Lys
275 280 285

Lys Pro Lys Arg Gly Thr Cys Thr Lys Gln Gly Gly Asn Thr Asn Ala
290 295 300

Ser Val Thr Asp Glu Glu Glu His Gly Asn Ile Leu Pro Lys Leu Asn
305 310 315 320

Ile Glu His Gly Glu Lys Val Asn Trp Leu Leu Gly Thr Lys Ile Lys
325 330 335

Gly His Gln Asn Ile Leu Val Ala Asp Gln Thr Ser Cys Ile Ser Val
340 345 350

Tyr Pro Leu Asn Glu Phe
355

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:


```

CCGGAGGTAG CTACCACGGC CTGTGTCAAC GACTAAAGCT CCAGTACAGC GGCGCCCTCA 60
GACAGCTGGG AGGGTGGCTC TGGCCGGGAG CGGCGGCCGG TGAGCTACCG CGAGGAGGAG 120
CGGCGGAGGC GACCTCGGCC CGGCCCTGCA CTGGCCGCCC GGCAGGCGCG ACATGAGCCT 180
GGTCTGGCAT CCGCGGGATG CTCCTTAAGC CCCTTCTCCG GCTGTTAACC TCCGGGGAAC 240
GGTTGTGACC ACACCGACAC GTATTTTACA GATAAATCAT TCTTGCGGCG GCGGGTCGAA 300
CACGTTTATT TATTTTTTAT TTTCTCAACA AGCTTTTACC CAGCACCTGT CCAGTGAAAC 360
AACTTGATAA TCGTTTCGAG GGGCGTCCGC CGGGTTAGGA AGCCACTGCC TGGCAGCTTG 420
TGGAAGCCTC ATTTGCAAAG CCACCCCTCA GATGTTTGA AGATCGTGAC GTCTTGTAAC 480
TAGCAGTGTG TGCACAGAAT CCTACTCAAG GAACGTCTTG GCCCAGCGAT GCAAAGAACT 540
GAAGTTTCAA GCTGGAAGAG CCTGTATTGT CCTCACAATA GTATAGAAGA ATTCAGAGA 600
GGAGAGAGAG ACAGCACCGA ATGAAGACTG TAAAAGAAAA GAAGGAATGC CAGAGATTGA 660
GAAAATCTGC CAAGACTAGG AGGGTAACCC AGAGGAAACC GTCTTCAGGG CCTGTTTGCT 720
GGCTATGCCT TCGAGAACCT GGGGATCCCG AAAAATTAGG GGAATTTCTT CAGAAAGACA 780
ATATCAGCGT GCATTATTTC TGTCTTATCT TATCTAGTAA GCTGCCTCAG AGGGGCCAGT 840
CCAACAGAGG TTTCCATGGA TTTCTGCCTG AAGACATCAA AAAGGAGGCA GCCCGGGCTT 900
CTAGGAAGAT CTGCTTTGTG TGCAAGAAAA AGGGAGCTGC TATCAACTGC CAGAAGGATC 960
AGTGCCTCAG AAACCTCCAT CTGCCTTGTC GCCAAGAAAG GGGTTGCCTT TCACAATTTT 1020
TTGGAGAGTA CAAATCATTT TGTGACAAAC ATCGCCCAAC ACAGAACATC CAACATGGGC 1080
ATGTGGGGGA GGAAAGCTGC ATCTTATGTT GTGAAGACTT ATCCAACAG AGTGTTGAGA 1140
ACATCCAGAG CCCGTGTTGT AGTCAAGCCA TCTACCACCG CAAGTGCATA CAGAAATATG 1200
CCCACACATC AGCAAAGCAT TTCTTCAAT GTCCACAGTG TAACAATCGA AAAGAGTTTC 1260
CTCAAGAAAT GCTGAGAATG GGAATTCATA TTCCAGACAG AGATGCTGCC TGGGAACTCG 1320
AGCCAGGGGC TTTCTCAGAC TTATATCAGC GCTATCAGCA CTGTGATGCC CCCATCTGTC 1380
CGTATGAACA AGGCAGAGAC AGCTTTGAGG ATGAAGGGAG GTGGTGCCTC ATTCTGTGTG 1440
CTACATGCGG ATCCCACGGA ACCCAGAGG ACTGCTCCTC TCTTAGATTT AACAGTAAGA 1500
AATGGGAGTG TGAGGAGTGT TCACCTGCTG CAGCCACAGA CTACATACCT GAAAACTCAG 1560
GGGACATCCC TTGCTGCAGC AGCACCTTCC ACCCTGAGGA ACATTTCTGC AGAGACAACA 1620
CCTTGGAAGA GAATCCGGGC CTTTCTTGGA CTGATTGGCC AGAACCTTCC TTATTAGAAA 1680
AGCCAGAGTC CTCTCGTGGC AGGAGGAGCT ACTCCTGGAG GTCCAAGGGT GTCAGAATCA 1740
CTAACAGCTG CAAAAAATCC AAGTAACACC TTCTGAGTAG CTGCTGTCCC ACACAATAGG 1800
GTATGAAGCT GCGCTCCTCC ATCGGGTTTG GGGAGGGAGC ACTCTGGGAC TGTGAGACAA 1860
GGAAGCAGGG CCAGCAGTGA GACTATGAGC CAAGCAAAGA GAAGTCTCAG TGGAGCATGA 1920
GGAGGGAGCA GTCCAGATGC CAACAAGGAA ATGCGTTTAT GGCTACAAGA GTGCCCTCTGC 1980
TTTCTCCTCC TCTCCTCCCA CCAAGGATTC TTCCACCTTA ATCTTGTTTT CATATGCCCTC 2040
TTCTTACTTC ACCCATGTTT GTTGTTATGC AAATAAAGGT TTTCTCTCCC AAAAAAAAAA 2100
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 2132

```

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

Met Lys Thr Val Lys Glu Lys Lys Glu Cys Gln Arg Leu Arg Lys Ser
 1             5             10             15
Ala Lys Thr Arg Arg Val Thr Gln Arg Lys Pro Ser Ser Gly Pro Val
          20             25             30
Cys Trp Leu Cys Leu Arg Glu Pro Gly Asp Pro Glu Lys Leu Gly Glu
          35             40             45
Phe Leu Gln Lys Asp Asn Ile Ser Val His Tyr Phe Cys Leu Ile Leu
          50             55             60

```

Ser Ser Lys Leu Pro Gln Arg Gly Gln Ser Asn Arg Gly Phe His Gly
 65 70 75 80
 Phe Leu Pro Glu Asp Ile Lys Lys Glu Ala Ala Arg Ala Ser Arg Lys
 85 90 95
 Ile Cys Phe Val Cys Lys Lys Lys Gly Ala Ala Ile Asn Cys Gln Lys
 100 105 110
 Asp Gln Cys Leu Arg Asn Phe His Leu Pro Cys Gly Gln Glu Arg Gly
 115 120 125
 Cys Leu Ser Gln Phe Phe Gly Glu Tyr Lys Ser Phe Cys Asp Lys His
 130 135 140
 Arg Pro Thr Gln Asn Ile Gln His Gly His Val Gly Glu Glu Ser Cys
 145 150 155 160
 Ile Leu Cys Cys Glu Asp Leu Ser Gln Gln Ser Val Glu Asn Ile Gln
 165 170 175
 Ser Pro Cys Cys Ser Gln Ala Ile Tyr His Arg Lys Cys Ile Gln Lys
 180 185 190
 Tyr Ala His Thr Ser Ala Lys His Phe Phe Lys Cys Pro Gln Cys Asn
 195 200 205
 Asn Arg Lys Glu Phe Pro Gln Glu Met Leu Arg Met Gly Ile His Ile
 210 215 220
 Pro Asp Arg Asp Ala Ala Trp Glu Leu Glu Pro Gly Ala Phe Ser Asp
 225 230 235 240
 Leu Tyr Gln Arg Tyr Gln His Cys Asp Ala Pro Ile Cys Pro Tyr Glu
 245 250 255
 Gln Gly Arg Asp Ser Phe Glu Asp Glu Gly Arg Trp Cys Leu Ile Leu
 260 265 270
 Cys Ala Thr Cys Gly Ser His Gly Thr His Arg Asp Cys Ser Ser Leu
 275 280 285
 Arg Phe Asn Ser Lys Lys Trp Glu Cys Glu Glu Cys Ser Pro Ala Ala
 290 295 300
 Ala Thr Asp Tyr Ile Pro Glu Asn Ser Gly Asp Ile Pro Cys Cys Ser
 305 310 315 320
 Ser Thr Phe His Pro Glu Glu His Phe Cys Arg Asp Asn Thr Leu Glu
 325 330 335
 Glu Asn Pro Gly Leu Ser Trp Thr Asp Trp Pro Glu Pro Ser Leu Leu
 340 345 350
 Glu Lys Pro Glu Ser Ser Arg Gly Arg Arg Ser Tyr Ser Trp Arg Ser
 355 360 365
 Lys Gly Val Arg Ile Thr Asn Ser Cys Lys Lys Ser Lys
 370 375 380

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

GTCACGTGGA ACCTCTTAAT CTCAGCATCC GGAGCTCCAG GAAGGGAAAA TTTCAAGTCA 60
GATAGAATTC TATATATACC ATTTCTTTGG AACCTTCAGC CCTCAAGATT CCAACATCAT 120
GACCTCAGTT TCAACACAGT TGTCTTAGT CCTCATGTCA CTGCTTTTGG TGCTGCCTGT 180
TGTGGAAGCA GTAGAAGCCG GTGATGCAAT CGCCCTTTTG TTAGGTGTGG TTCTCAGCAT 240
TACAGGCATT TGTGCCTGCT TGGGGGTATA TGCACGAAAA AGAAATGGAC AGATGTGACT 300
TTGAAAGGCC TACTGAGTCA AACCTCACCC TGAAACCTT TGCCTTTAG AGGCTAAACC 360
TGAGATTTGG TGTGTGAAAG GTTCCAAGAA TCAGTAAATA AGGGAGTTTC ACATTTTTC 420
TTGTTTCCAT GAAATGGCAA CAAACATACA TTTATAAATT GAAAAAAAAA TGTTTCTTT 480
ACAACAAATA ATGCACAGAA AAATGCAGCC TATAATTTGC TAGTTAGGTA GTCAAAGAAG 540
TAAGATGGCT GAAATTTACA TAAGTAATAT TTCATAATCT TAGAATTCTC TCAAAGCATG 600
TGAAATAGGA AGAAGGAAGT TCTTGCCCAG AATCTTAGGA AATCACCCT GTTCGGTTAT 660
AATCACTGCC TCCTGAATCG TTGAGGAGTC TTTTAAATTA GATTTTGTG TTGTTGTCTC 720
CCAAGTTAAT ATTATATTTA GATATCAGAG AGTCAGGCAA AAAGGAAAAC TTTTATCTCT 780
AGGGAAAAAA CATTTAGAAA AATGTATTCA GTGTATCTAA TACTGAAATG CGGAAAAAAA 840
TTTAATGTTA AAAAAAACT ATAGACATTG ACATGGAAAA GAGATTTAAT GTTTTGAAAA 900
AAAAACTTTA TATTAACCTG GTAACATCCT CCTGATGAGA AGTACTATAT TAAATATAAA 960
CCCATTATGT TATAAAAAAA AAAA                                     984

```

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu
 1              5              10              15
Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala
              20              25              30
Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Cys Ala Cys Leu
              35              40              45
Gly Val Tyr Ala Arg Lys Arg Asn Gly Gln Met
              50              55

```

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GTTCCTACAG CGGTGAGAGT GAAATGTG

28

- (2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

CCGATACACC AAAGTCTCAT CCCTAAAT

28

- (2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAGCTAGTGT GAAGGACAAAT AAGCAGAA

28

- (2). INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GTCGCTAACA TCAGAACTAA CAGATTCA

28

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAGATACTGC AAATGAATTT ACACGGGT

28

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GTCACACTTA ACTCCCATCA CCCGAAAG

28

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCTGAGGCAC TGATCCTTCT GGCAGTTG

28

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TGAGGGCTGA AGGTTCCAAA GAAATGGT

28

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

```

CGCTTTTTTT TTTTTTTTGA CAAGATGGCG GCAGGAGGCA GTGGCGTTGG TGGGAAGCGC 60
AGCTCGAAAA GCGATGCCGA TTCTGGTTTC CTGGGGCTGC GGCCCACTTC GGTGGACCCA 120
GCGCTGAGGC GCGGCGGCG AGGCCCAAGA AATAAGAAGC GGGGCTGGCG GCGGCTTGCT 180
CAGGAGCCGC TGGGGCTGGA GGTGACCAG TTCCTGGAAG ACGTGC GGCT ACAGGAGCGC 240
ACGAGCGGTG GCTTGTTGTC AGAGGCCCCA AATGAAAAAC TCTTCTTCGT GGACACTGGC 300
TCCAAGGAAA AAGGGCTGAC AAAGAAGAGA ACCAAAGTCC AGAAGAAGTC ACTGCTTCTC 360
AAGAAACCCC TTCGGGTTGA CCTCATCCTC GAGAACACAT CCAAAGTCCC TGCCCCCAAA 420
GACGTCCTCG CCCACCAGGT CCCCACGCC AAGAAGCTCA GGCGGAAGGA GCAGCTATGG 480
GAGAAGCTGG CCAAGCAGGG CGAGCTGCCC CGGGAGGTGC GCAGGGCCCA GGCCCGGCTC 540
CTCAACCCTT CTGCAACAAG GGCCAAGCCC GGGCCCCAGG ACACCGTAGA GCGGCCCTTC 600
TACGACCTCT GGGCCTCAGA CAACCCCCTG GACAGGCCGT TGGTTGGCCA GGATGAGTTT 660
TTCCTGGAGC AGACCAAGAA GAAAGGAGTG AAGCGGCCAG CACGCCTGCA CACCAAGCCG 720
TCCCAGGCGC CCGCCGTGGA GGTGGCGCCT GCCGGAGCTT CCTACAATCC ATCCTTTGAA 780
GACCACCAGA CCCTGCTCTC AGCGGCCAC GAGGTGGAGT TGCAGCGGCA GAAGGAGGCG 840
GAGAAGCTGG AGCGGCAGCT GGCCCTGCCC GCCATGGAGC AGGCCGCCAC CCAGGAGTCC 900
ACATTCCAGG AGCTGTGCGA GGGGCTGCTG GAGGAGTCGG ATGGTGAGGG GGAGCCAGGC 960
CAGGGCGAGG GGCCGGAGGC TGGGGATGCC GAGGTCTGTC CCACGCCCCG CCGCCTGGCC 1020
ACCACAGAGA AGAAGACGGA GCAGCAGCGG CGGCGGGAGA AGGCTGTGCA CAGGCTGCGG 1080
GTACAGCAGG CCGCGTTGCG GGCCGCCCGG CTCCGGCACC AGGAGCTGTT CCGGCTGCGC 1140
GGGATCAAGG CCCAGGTGGC CCTGAGGCTG GCGGAGCTGG CGCGGCGGCG GAGGCGGCGG 1200
CAGGCGCGGC GGGAGGCTGA GGCTGACAAG CCCCGAAGGC TGGGACGGCT CAAGTACCAG 1260
GCACCTGACA TCGACGTGCA GCTGAGCTCG GAGCTGACAG ACTCGCTCAG GACCCTGAAG 1320
CCCGAGGGCA ACATCCTTCG AGACCGGTTT AAGAGCTTCC AGAGGAGGAA TATGATCGAG 1380
CCTCGAGAGA GAGCCAAGTT CAAACGCAAG TACAAGGTGA AGCTGGTGGA GAAGCGGGCG 1440
TTCCGTGAGA TCCAGTTGTA GCTGCCATCA GATGCCGGAG ACTCGCCCTT CAATAAAAAA 1500
TCTCTTCTAG CTGAAAAAAA AAAAAAAA 1528

```

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

```

Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg Ser Ser Lys Ser
 1             5             10             15
Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr Ser Val Asp Pro
          20             25             30
Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp
          35             40             45

```

Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu
50 55 60

Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu
65 70 75 80

Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys
85 90 95

Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu
100 105 110

Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val
115 120 125

Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys
130 135 140

Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu
145 150 155 160

Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser
165 170 175

Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe
180 185 190

Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly
195 200 205

Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg
210 215 220

Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val
225 230 235 240

Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr
245 250 255

Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala
260 265 270

Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Met Glu Gln Ala Ala
275 280 285

Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu
290 295 300

Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly
305 310 315 320

Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala Thr Thr Glu Lys
325 330 335

Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val His Arg Leu Arg
340 345 350

Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg His Gln Glu Leu
355 360 365

Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu

370	375	380
Leu Ala Arg Arg Arg Arg Arg Arg Gln Ala Arg Arg Glu Ala Glu Ala		
385	390	395 400
Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile		
	405	410 415
Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys		
	420	425 430
Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg		
	435	440 445
Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys		
	450	455 460
Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu		
465	470	475

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

ACAAGATGGC	GGCGCCGAAG	GGGAGCCTCT	GGGTGAGGAC	CCAAGTGGGG	CTCCCGCCGC	60
TGCTGCTGCT	GACCATGGCC	TTGGCCGGAG	GTTGCGGGAC	CGCTTCGGCT	GAAGCATTTG	120
ACTCGGTCTT	GGGTGATACG	GCGTCTTGCC	ACCGGGCCTG	TCAGTTGACC	TACCCCTTGC	180
ACACCTACCC	TAAGGAAGAG	GAGTTGTACG	CATGTCAGAG	AGGTTGCAGG	CTGTTTTCAA	240
TTTGTCAGTT	TGTGGATGAT	GGAATTGACT	TAAATCGAAC	TAAATTGGAA	TGTGAATCTG	300
CATGTACAGA	AGCATATTCC	CAATCTGATG	AGCAATATGC	TTGCCATCTT	GGTTGCCAGA	360
ATCAGCTGCC	ATTCGCTGAA	CTGAGACAAG	AACAACCTAT	GTCCCTGATG	CCAAAAATGC	420
ACCTACTCTT	TCCTCTAACT	CTGGTGAGGT	CATTCTGGAG	TGACATGATG	GACTCCGCAC	480
AGAGCTTCAT	AACCTCTTCA	TGGACTTTT	ATCTTCAAGC	CGATGACGGA	AAAATAGTTA	540
TATTCCAGTC	TAAGCCAGAA	ATCCAGTACG	CACCACATTT	GGAGCAGGAG	CCTACAAATT	600
TGAGAGAATC	ATCTCTAAGC	AAAATGTCCT	CAGATCTGCA	AATGAGAAAT	TCACAAGCGC	660
ACAGGAATTT	TCTTGAAGAT	GGAGAAAGTG	ATGGCTTTTT	AAGATGCCTC	TCTCTTAACT	720
CTGGGTGGAT	TTTAACTACA	ACTCTTGTC	TCTCGGTGAT	GGTATTGCTT	TGGATTGTGT	780
GTGCAACTGT	TGCTACAGCT	GTGGAGCAGT	ATGTTCCCTC	TGAGAAGCTG	AGTATCTATG	840
GTGACTTGGA	GTTTATGAAT	GAACAAAAGC	TAAACAGATA	TCCAGCTTCT	TCTCTTGTTG	900
TTGTTAGATC	TAAAAGTAA	GATCATGAAG	AAGCAGGGCC	TCTACCTACA	AAAGTGAATC	960
TTGCTCATT	TGAAATTTAA	GCATTTTCT	TTTAAAAGAC	AAGTGTAAAT	GACATCTAAA	1020
ATTCCACTCC	TCATAGAGCT	TTTAAAATGG	TTTCATTGGA	TATAGGCCTT	AAGAAATCAC	1080
TATAAAATGC	AAATAAAGTT	ACTCAAATCT	GTGAAGACTG	TATTTGCTAT	AACTTTATTG	1140
GTATTGTTTT	TGTAGTAATT	TAAGAGGTGG	ATGTTTGGA	TTGTATTATT	ATTTTACTAA	1200
TATCTGTAGC	TATTTTGTTT	TTTGCTTTGG	TTATTGTTTT	TTTCCCTTTT	CCTAGCTATG	1260
AGCTGATCAT	TGCTCCTTCT	CACCTCCTGC	CATGATACTG	TCAGTTACCT	TAGTTAACAA	1320
GCTGAATATT	TAGTAGAAAT	GATGCTTCTG	CTCAGGAATG	GCCCACAAAT	CTGTAATTTG	1380
AAATTTAGCA	GGAAATGACC	TTTAATGACA	CTACATTTTC	AGGAACTGAA	ATCATTAATA	1440
TTTTATTGTA	ATAATTAAAA	AAAAAAAAAA	AA			1472

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu
 1           5           10           15
Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr
          20           25           30
Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys
          35           40           45
His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu
          50           55           60
Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys
          65           70           75           80
Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys
          85           90           95
Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
          100          105          110
Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
          115          120          125
Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
          130          135          140
Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
          145          150          155          160
Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys
          165          170          175
Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu
          180          185          190
Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser
          195          200          205
Ser Asp Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu
          210          215          220
Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly
          225          230          235          240
Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp
          245          250          255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro Ser
          260          265          270

```

Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu Gln Lys
275 280 285

Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg Ser Lys Thr
290 295 300

Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn Leu Ala
305 310 315 320

His Ser Glu Ile

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GTGATTGGTA	CAGTAGGTTT	ATAAACAGAA	GTTTAAACTT	GTAAGCTTAA	GCTTCCGTTT	60
ATAAACAGAA	GTTTAAAATT	ATAGGTCCTG	TTTAACATTC	AGCTCTGTTA	ACTCACTCAT	120
CTTTTGTGT	TTTACACTT	TGTCAAGATT	TCTTTACATA	TTCATCAATG	TCTGAAGAAG	180
TTACTTATGC	AGATCTTCAA	TTCCAGAACT	CCAGTGAGAT	GGAAAAAATC	CCAGAAATTG	240
GCAAATTTGG	GGAAAAAGCA	CCTCCAGCTC	CCTCTCATGT	ATGGCGTCCA	GCAGCCTTGT	300
TTCTGACTCT	TCTGTGCCTT	CTGTTGCTCA	TTGGATTGGG	AGTCTTGGA	AGCATGTTTC	360
ATGTAACCTT	GAAGATAGAA	ATGAAAAAAA	TGAACAACT	ACAAAACATC	AGTGAAGAGC	420
TCCAGAGAAA	TATTTCTCTA	CAACTGATGA	GTAACATGAA	TATCTCCAAC	AAGATCAGGA	480
ACCTCTCCAC	CACACTGCAA	ACAATAGCCA	CCAAATTATG	TCGTGAGCTA	TATAGCAAAG	540
AACAAGAGCA	CAAATGTAAG	CCTTGTCCTA	GGAGATGGAT	TTGGCATAAG	GACAGCTGTT	600
ATTTCTAAG	TGATGATGTC	CAAACATGGC	AGGAGAGTAA	AATGGCCTGT	GCTGCTCAGA	660
ATGCCAGCCT	GTTGAAGATA	AACAACAAAA	ATGCATTGGA	ATTTATAAAA	TCCCAGAGTA	720
GATCATATGA	CTATTGGCTG	GGATTATCTC	CTGAAGAAGA	TTCCACTCGT	GGTATGAGAG	780
TGGATAATAT	AATCCACTCC	TCTGCCTGGG	TTATAAGAAA	CGCACCTGAC	TTAAATAACA	840
TGTATTGTGG	ATATATAAAT	AGACTATATG	TTCAATATTA	TCACTGCACT	TATAAACAAA	900
GAATGATATG	TGAGAAGATG	GCCAATCCAG	TGCAGCTTGG	TTCTACATAT	TTTAGGGAGG	960
CATGAGGCAT	CAATCAAATA	CATTGAAGGA	GTGTAGGGGG	TGGGGGTTCT	AGGCTATAGG	1020
TAAATTTAAA	TATTTTCTGG	TTGACAATTA	GTTGAGTTTG	TCTGAAGACC	TGGGATTTTA	1080
TCATGCAGAT	GAAACATCCA	GGTAGCAATG	TTGAGAGAGA	ATAGACTGTG	AATGTTAATG	1140
CCAGAGAGGT	ATAATGAAGC	ATGTCCMACY	TCCCACTTTC	CATCATGGCY	TGAACCYKGG	1200
RGGAAGAGGA	AGTCCATTCA	GATAGTTGTG	GGGGGCCCTT	GAATTTTCAT	TTTCATWWAC	1260
GTTCTTCCCC	TTCTGGCCAA	GATTTGCCAG	AGGCAACATC	AAAAACCAGC	AAATTKTAAT	1320
TTTGTCCCAC	AGSGTTGCTA	GGGTGGCATG	GYTCCCCATT	TSGGGTCCAT	CCTAWACTTC	1380
CATGGGACTC	CCTATGGCTG	AAGGCCTTAT	GAGTCAAAGG	ACTTATAGCC	AATTGATTGT	1440
TTTAGGCCAG	GTAAGAATGG	ATATGGACAT	GCATTTATTA	CYTYTTAAAA	TTATTATTTT	1500
AAGTAAAAGC	CAATAAACAA	AAANGNAAAG	GCAAAAAAAA	AAAAA	AAAAA	1560
AAAAA	AAA					1573

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Met	Ser	Glu	Glu	Val	Thr	Tyr	Ala	Asp	Leu	Gln	Phe	Gln	Asn	Ser	Ser		
1				5					10					15			
Glu	Met	Glu	Lys	Ile	Pro	Glu	Ile	Gly	Lys	Phe	Gly	Glu	Lys	Ala	Pro		
		20						25					30				
Pro	Ala	Pro	Ser	His	Val	Trp	Arg	Pro	Ala	Ala	Leu	Phe	Leu	Thr	Leu		
		35					40					45					
Leu	Cys	Leu	Leu	Leu	Leu	Ile	Gly	Leu	Gly	Val	Leu	Ala	Ser	Met	Phe		
	50					55					60						
His	Val	Thr	Leu	Lys	Ile	Glu	Met	Lys	Lys	Met	Asn	Lys	Leu	Gln	Asn		
65					70					75				80			
Ile	Ser	Glu	Glu	Leu	Gln	Arg	Asn	Ile	Ser	Leu	Gln	Leu	Met	Ser	Asn		
				85					90					95			
Met	Asn	Ile	Ser	Asn	Lys	Ile	Arg	Asn	Leu	Ser	Thr	Thr	Leu	Gln	Thr		
			100					105					110				
Ile	Ala	Thr	Lys	Leu	Cys	Arg	Glu	Leu	Tyr	Ser	Lys	Glu	Gln	Glu	His		
		115					120					125					
Lys	Cys	Lys	Pro	Cys	Pro	Arg	Arg	Trp	Ile	Trp	His	Lys	Asp	Ser	Cys		
	130					135					140						
Tyr	Phe	Leu	Ser	Asp	Asp	Val	Gln	Thr	Trp	Gln	Glu	Ser	Lys	Met	Ala		
145					150					155					160		
Cys	Ala	Ala	Gln	Asn	Ala	Ser	Leu	Leu	Lys	Ile	Asn	Asn	Lys	Asn	Ala		
				165					170					175			
Leu	Glu	Phe	Ile	Lys	Ser	Gln	Ser	Arg	Ser	Tyr	Asp	Tyr	Trp	Leu	Gly		
		180						185					190				
Leu	Ser	Pro	Glu	Glu	Asp	Ser	Thr	Arg	Gly	Met	Arg	Val	Asp	Asn	Ile		
		195					200					205					
Ile	His	Ser	Ser	Ala	Trp	Val	Ile	Arg	Asn	Ala	Pro	Asp	Leu	Asn	Asn		
	210				215					220							
Met	Tyr	Cys	Gly	Tyr	Ile	Asn	Arg	Leu	Tyr	Val	Gln	Tyr	Tyr	His	Cys		
225					230					235					240		
Thr	Tyr	Lys	Gln	Arg	Met	Ile	Cys	Glu	Lys	Met	Ala	Asn	Pro	Val	Gln		
			245						250					255			
Leu	Gly	Ser	Thr	Tyr	Phe	Arg	Glu	Ala									
			260				265										

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAGTTATATG	ACACTCAAAG	GAAAAGCAAA	AGAGCATTAA	GAAGTGTCTG	TTTTTGTTAT	60
TGCCATTTCA	TAAATATTTT	AGTAGGTGTT	CAATTCATT	GGATATTCTT	TTTTTTAAT	120
TGTCTTTGTA	CCTATGATTG	AAAACAGTAG	TTGGTCTATG	ACTTTTGAGG	AGAGGGAGAA	180
CCGAAGATTA	CAGGAGGCCA	GCATGAGGTT	GGAACAAGAG	AATGATGACC	TTGCCCATGA	240
ACTAGTAACA	AGCAAAATTG	CTCTACGGAA	TGACTTGGAT	CAGGCAGAAG	ACAAGGCAGA	300
TGTGTTGAAT	AAAGAGCTCC	TTTTGACCAA	ACAGAGGCTG	GTGGAGACTG	AAGAGGAGAA	360
GAGGAAGCAA	GAGGAAGAGA	CTGCCCAGCT	AAAAGAAGTC	TTCAGGAAAC	AGCTAGAGAA	420
GGCAGAATAT	GAAATAAAGA	AGACTACAGC	TATCATTGCT	GAGTATAAAC	AGGTAATGTA	480
CTTCTGTGGC	ACATAGAGCT	AGTTATAGTT	TGCTGCTATA	AAAGTAATTT	TTTTTTTTTT	540
TTGCTTGAGG	CCAGGAGTTT	GAGACTAGCC	TGAGCAACAT	AGCAGGACTC	CGTCCCAAGG	600
AAAAAAAAAA	AAAAAAAA					618

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met	Ile	Glu	Asn	Ser	Ser	Trp	Ser	Met	Thr	Phe	Glu	Glu	Arg	Glu	Asn
1			5					10					15		
Arg	Arg	Leu	Gln	Glu	Ala	Ser	Met	Arg	Leu	Glu	Gln	Glu	Asn	Asp	Asp
		20					25						30		
Leu	Ala	His	Glu	Leu	Val	Thr	Ser	Lys	Ile	Ala	Leu	Arg	Asn	Asp	Leu
		35				40						45			
Asp	Gln	Ala	Glu	Asp	Lys	Ala	Asp	Val	Leu	Asn	Lys	Glu	Leu	Leu	Leu
	50				55					60					
Thr	Lys	Gln	Arg	Leu	Val	Glu	Thr	Glu	Glu	Glu	Lys	Arg	Lys	Gln	Glu
65				70					75					80	
Glu	Glu	Thr	Ala	Gln	Leu	Lys	Glu	Val	Phe	Arg	Lys	Gln	Leu	Glu	Lys
			85					90					95		
Ala	Glu	Tyr	Glu	Ile	Lys	Lys	Thr	Thr	Ala	Ile	Ile	Ala	Glu	Tyr	Lys
		100					105						110		
Gln	Val	Met	Tyr	Phe	Cys	Gly	Thr								
		115					120								

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TGCAGAATCC	AGAATGGATG	TCCTCTTTGT	AGCCATCTTT	GCTGTGCCAC	TTATCCTGGG	60
ACAAGAATAT	GAGGATGAAG	AAAGACTGGG	AGAGGATGAA	TATTATCAGG	TGGTCTATTA	120
TTATACAGTC	ACCCCCAGTT	ATGATGACTT	TAGTGCAGAT	TTCACCATTG	ATTACTCCAT	180
ATTTGAGTCA	GAGGACAGGC	TGAACAGGTT	GGATAAGGAC	ATAACAGAAG	CAATAGAGAC	240
TACCATTAGT	CTTGAAACAG	CACGTGCAGA	CCATCCGAAG	CCTGTAACTG	TGAAACCAGT	300
AACAACGGAA	CCTAGTCCAG	ATCTGAACGA	TGCCGTGTCC	AGTTTGCGAA	GTCTTATTC	360
CCTCCTCCTG	TCGTGTGCCT	TTGTTTCAGT	GGGGATGTAT	TTCATGTAGA	AGGTGGAAGA	420
AGGCTGCTAT	GACTCTTTGG	ATGGGAGTCT	GGCAAGAGGA	AATTGGAAGA	TAAAATAAAT	480
AATAAGTGAA	ATAAAAAAAA	AAAAA				510

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly
1      5      10      15
Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
20     25     30
Val Val Tyr Tyr Thr Val Thr Pro Ser Tyr Asp Asp Phe Ser Ala
35     40     45
Asp Phe Thr Ile Asp Tyr Ser Ile Phe Glu Ser Glu Asp Arg Leu Asn
50     55     60
Arg Leu Asp Lys Asp Ile Thr Glu Ala Ile Glu Thr Thr Ile Ser Leu
65     70     75     80
Glu Thr Ala Arg Ala Asp His Pro Lys Pro Val Thr Val Lys Pro Val
85     90     95
Thr Thr Glu Pro Ser Pro Asp Leu Asn Asp Ala Val Ser Ser Leu Arg
100    105    110
Ser Pro Ile Pro Leu Leu Leu Ser Cys Ala Phe Val Gln Val Gly Met
115    120    125
Tyr Phe Met
130

```

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 883 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

CATCTGACCA TCCATATCCA ATGTTCTCAT TTAAACATTA CCCAGCATCA TTGTTTATAA      60
TCAGAACTC TGGTCCTTCT GTCTGGTGGC ACTTAGAGTC TTTTGTGCCA TAATGCAGCA      120
GTATGGAGGG AGGATTTTAT GGAGAAATGG GGATAGTCTT CATGACCACA AATAAATAAA      180
GGAAACTAA GCTGCATTGT GGGTTTTGAA AAGGTTATTA TACTTCTTAA CAATTCCTTT      240
TTTCAGGGAC TTTTCTAGCT GTATGACTGT TACTTGACCT TCTTTGAAAA GCATTCCCAA      300
AATGCTCTAT TTTAGATAGA TTAACATTAA CCAACATAAT TTTTTTTAGA TCGAGTCAGC      360
ATAAATTTCT AAGTCAGCCT CTAGTCGTGG TTCATCTCTT TCACCTGCAT TTTATTTGGT      420
GTTTGTCTGA AGAAAGGAAA GAGGAAAGCA AATACGAATT GTACTATTTG TACCAAATCT      480
TTGGGATTCA TTGGCAAATA ATTTCAAGTGT GGTGTATTAT TAAATAGAAA AAAAAAATTT      540
TGTTTCCTAG GTTGGAAGGC TAATTGATAC GTTTGACTTA TGATGACCAT TTATGCACTT      600
TCAAATGAAT TTGCTTTCAA AATAAATGAA GAGCAGCTGT CCTTCTTTCC TCTTTTAAGT      660
GTTCACTGT GGCATGCTCA GAGGTTCTTG CTGGATTCCA GCTGGAGCGG TGTGATACCC      720
TTCTTTTTC GCTGTTCTGT CCTTCCTTTC TTGTATCCAC CAAAGTGGAG ACAAATACAT      780
GATCTCAAAG ATACACAGTA CCTACTTAAT TCCAGCTGAT GGGAGACCAA AGAATTTGCA      840
AGTGGATGGT TTGGTATCAC TGTAATAAAA AAGAGGGCCT GGG                        883

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(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Met Met Thr Ile Tyr Ala Leu Ser Asn Glu Phe Ala Phe Lys Ile Asn

1	5	10	15
Glu Glu Gln Leu Ser Phe Phe Pro Leu Leu Ser Val Gln Leu Trp His			
	20	25	30
Ala Gln Arg Phe Leu Leu Asp Ser Ser Trp Ser Gly Val Ile Pro Phe			
	35	40	45
Phe Phe Ser Cys Ser Cys Leu Pro Phe Leu Tyr Pro Pro Lys Trp Arg			
	50	55	60
Gln Ile His Asp Leu Lys Asp Thr Gln Tyr Leu Leu Asn Ser Ser			
65	70	75	

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	110

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TAGGCCTCTT TGGCCGGTGC TGCCTGAGAA GGATTGGCAC GGGCACAGAC CACTGCCCCC	60
ACCTGCCCTG CGCCATCTAC CCAAGAAGGC TCGGCACGGG CACCAACCAC TGCCTCCAAC	120
TGCCCCATGC TGCCTGAGAA GGCACCTGCAC GGCCACCCCG AACTGCCCCG CACTGTCCCT	180
ACCCGGGCGAG CCATGCGAGC GGCTGGAAC CTGCTGGCCT TCTGCTGCCT GGTCTTGAGC	240
ACCACTGGGG GCCCTTCCCC AGATACTTGT TCCCAGGACC TTAACCTACG TGTGAAGCCA	300
GGATTTCTTA AAACAATAAA GACCAATGAC CCAGGAGTCC TCCAAGCAGC CAGATACAGT	360
GTTGAAAAGT TCAACAACCTG CACGAACGAC ATGTTCTTGT TCAAGGAGTC CCGCATCACA	420
AGGGCCCTAG TTCAGATAGT GAAAGGCCTG AAATATATGC TCGARGTGGA AATTGGCAGA	480
ACTACCTGCA AGAAAAACCA GCACCTGCGT CTGGATGACT GTGACTTCCA AACCAACCAC	540
ACCTTGAAGC AGACTCTGAG CTGCTACTCT GAAGTCTGGG TCGTGCCCTG GCTCCAGCAC	600
TTCGAGGTGC CTGTTCTCCG TTGTCACTGA CCCCCGCCTC TTCAGCAAGA CCACAGCCAT	660
GACAAACACC AGGATGCATG CTCCTTGTC CCTCCCACCC GCYWSRTGAC CRRRCCTSAC	720
AGACCCTCTC RGGCCTCWGA CGAGTGAGCG GRTGAAGTGC MAYTGGGTSA CMGCAGGGCA	780
GCTRGAATGG CAGCWTGGTA GCGCCTCCTA ACAGRTTAAA TRGATCACAT GTGMTTCTAA	840
AATTAAAAA AAAAAAAAAA A	861

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Met 1	Leu	Pro	Glu	Lys 5	Ala	Leu	His	Gly	His 10	Pro	Gln	Leu	Pro	Arg 15	Thr
Val	Pro	Thr	Arg 20	Ala	Ala	Met	Arg	Ala 25	Ala	Gly	Thr	Leu	Leu	Ala 30	Phe
Cys	Cys	Leu	Val	Leu	Ser	Thr	Thr 40	Gly	Gly	Pro	Ser	Pro 45	Asp	Thr	Cys
Ser	Gln 50	Asp	Leu	Asn	Ser	Arg 55	Val	Lys	Pro	Gly	Phe 60	Pro	Lys	Thr	Ile
Lys 65	Thr	Asn	Asp	Pro	Gly 70	Val	Leu	Gln	Ala 75	Ala	Arg	Tyr	Ser	Val	Glu 80
Lys	Phe	Asn	Asn 85	Cys	Thr	Asn	Asp	Met 90	Phe	Leu	Phe	Lys	Glu 95	Ser	Arg
Ile	Thr	Arg	Ala 100	Leu	Val	Gln	Ile	Val 105	Lys	Gly	Leu	Lys	Tyr 110	Met	Leu
Glu	Val	Glu 115	Ile	Gly	Arg	Thr	Thr 120	Cys	Lys	Lys	Asn	Gln 125	His	Leu	Arg
Leu	Asp 130	Asp	Cys	Asp	Phe	Gln 135	Thr	Asn	His	Thr	Leu 140	Lys	Gln	Thr	Leu
Ser 145	Cys	Tyr	Ser	Glu	Val 150	Trp	Val	Val	Pro	Trp 155	Leu	Gln	His	Phe	Glu 160
Val	Pro	Val	Leu	Arg 165	Cys	His									

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

ANCCAGAATC GGCATCGCTT TTCGAGCTG 29

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TNTGGTGCGT ACTGGATTTC TGGCTTAGA 29

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GNTAACAGAG CTGAATGTTA AACAGGACC

29

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TNTCCTCAAA AGTCATAGAC CAACTACTG

29

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GNTCAGCCTG TCCTCTGACT CAAATATGG

29

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TNACCTGCAT TTTATTTGGT GTTGTCTG

29

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TNAACACTGT ATCTGGCTGC TTGGAGGAC

29

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GCAAGATTTG GCCTGGATTC TTCTGAGGAT GTGAAGTAAT GGAAACAGTA AGACTGTTCC	60
AGACTAGGGG AAGACTAGAG ACCTAATAGC TGGATTCCAT GTGATCTTTT GTTGGACTTT	120
GGGATTGGAG GTGAGAGTAG AGAAGGCATA ATGCACGTTT TTGAGACGAG GGAAATGTGA	180
ATATAGCCTG TATGCCTACA CTCAAGTCTG AAGACATGTW AACCATGTCT ATACTAACCA	240
GCCAAATATT TGAACACTAA AAGGAAGAAT TTTCTTAATG TGGTAATGGT WTCATGGTTG	300
TATAGAATGT TCCTCCTCTT GGGAGATGTG TGTTGAAAAT AGGGTTTGAC GTCTAAACCT	360
ATTTTGT TTTT GGCAAAAAGG ACGTGTGTCT GTACAAAAGA AGTGGAGCCA GTATGGCAAA	420
ATGTTTACMA GGACTCTGGG TGAGARGTWC ATAGGTGCTT ACTATACTGT TTTGTTTCTG	480
AATTTGGAAT TTCTCAAAAT TAAAAAATA TCTACTGAGG AGCTTTTCGT TTAACTGGT	540
GGGGAATGGG TTCTGGGTGG TTTTGCCCCT TTTCTTTTGA GATTCAAGAA ATCCATGGTG	600
AAAGGTTTGG ATTCCTATGA AGAAAAGGAG GATAAAGTGA TCAAGGAGAT GGCAGCTCAG	660
ATCCGTGAGG TGGAGCAGAG CCGACAGGAG GTGGTTCGGT CTGTCTTAGA GGTGGTTTC	720
CCTCGGAGGA TCCAGACCAC CTCAGGCAGT GCCAGACCCA GAAGAGGGCT CTTCAGCACC	780
TAGAAGCTGG AAAGGGATGA ACAGGTAAGA CTATTAGGGA ATCTCTTGTT GGAATTTGA	840
CATCTTAGAA CATTCTGCAA CCTTTTGCCT GGGAAATGGA AACAGATCTA ATCTTTACCA	900
CCCTCATGGC TCAAGGACCT CATCTGGCAG CCTGGCTCAT GTTTTTCAGC CAAGTAGCTT	960
CCAGCTTACA GCAGCCCTCA AATTGACC TGCCACCAGC TCCAGAGCTT GACTGGATGG	1020
AGACAGGACC ATCTCTGACA TTCATTGGCC ATCAGGTACA AAGGATAAGC AAGCCAGAAG	1080
AGGGCCAATG GTCCCTCAGG TCTCAGGACC CCTTTCTCCT GATTTTCTAC CTATTCAAGC	1140
CACTGCTGCC TCCACTGCAG GCTTTTCCTT CTTCTTCAC TGTTCCCTAG TAGTGTCTC	1200

AGACCTCTTC TCACCCTCCA AAGCGATCCT ATTCACATGT ATTGACACTT AGGAGTGCCA	1260
ACTCCTAAAT CTTGCCCTCT GTAGAACTCA TAGTTCCAAC TCAACACAGG ACATTAAATA	1320
TCCCACAGGC ATCTGAAACT AACCCCCACC ACTCCTATAT TTCCAATCAC TAGATGCAGA	1380
TCCTTTTCTT TTCCATCTCC CATATCCTGT CAACAAGCGG TCAATTTTAA CCTGTCTGCC	1440
TCCATTCAGC CTTTGGGCAA TTTCTACTCC CCCTTCAATC CTGCCTCACA AACAGAAAAT	1500
CATTGTACCA CTTATGATTT TACTCTACAC TTCAGCTGTA TTGTGTTGCT TCGGGCTTTT	1560
GCAGTTGCCA TTGTCTAAAA CATGCTTTCC TTCCCTCATC ACCTAGTTTA CCTTCAACTG	1620
TTAGCTCAA TGTCACTTTT TCATAAAAGG CTTATCTGAA CAGGTTATCT CTATTTCAAG	1680
TGGATGTAGC ACCATGTAAA GTTGCAAATG TAATTTACGT AACTTGTGCT TAATGCTCTT	1740
CCCCAATTAT ATGTATGCTG TGAGGGCAAG GTTTTGCTCC CCTGGCATGT AATAGCCACT	1800
CTACTTACAG ACATCTCCAC TGTTATGACT GTGAGCTTCC TGAGGACAGG GTTGTCTTAG	1860
AGTGACTTAC TGTGCTTTCA AAGTTTAACA TCAGCTGGGG TGCAGAATTA GCATTGTGGC	1920
AGCAGTCACA CCCACCTCTT TTAAAGTGTG CTTTGTCTAT CGTTTCTAGG ATTTTTTTTT	1980
TTAATCATGC CTAGACTTTA ACTAGCACTT TTTTCCCAT TTCCAACAC AGGATATACC	2040
AGGAGTTGGT AACATCCACT CAGGTGCCAC ACCTCCCTGG ATGATCCAAG ATGAAGAATA	2100
CATTGCTGGG AACCAAGAAA TAGGACCATC CTATGAAGAA TTTCTTAAAG AAAAGGAAAA	2160
ACAGAAGTTG AAAAACTCC CCCCAGACCG AGTTGGGGCC AACTTTGATC ACAGCTCCAG	2220
GACCAGTGCA GGCTGGCTGC CCTCTTTTGG CCGTGTCTGG AATAATGGAC GCCGCTGGCA	2280
GTCCAGACAT CAATTCAAAA CTGAAGCTGC AGCAATGAAG AAGCAGTCAC ATACAGAAAA	2340
AAGCTAATCA TGCTCTCTAC CAACTACCAT GAGGCTAAAA GCAAAGTCAA CAAACCCCTA	2400
TTATACCTTC CACCAAATTC TTTATCATTG TCTTTCTTAG GAAACAGACA TACTCATTCA	2460
TTTGATTTAA TAAAGTTTAA TTTTCCAAA TGTACAGCTG GTTGGACCTG TAAAAAAAAA	2520
TTAAAGAAT CAGAACCATA AAAAAAAAAA AAAAAA	2556

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Met	Glu	Thr	Asp	Leu	Ile	Phe	Thr	Thr	Leu	Met	Ala	Gln	Gly	Pro	His
1				5					10					15	

Leu Ala Ala Trp Leu Met Phe Phe Ser Gln Val Ala Ser Ser Leu Gln
 20 25 30
 Gln Pro Ser Asn Leu Asp Leu Pro Pro Ala Pro Glu Leu Asp Trp Met
 35 40 45
 Glu Thr Gly Pro Ser Leu Thr Phe Ile Gly His Gln Val Gln Arg Ile
 50 55 60
 Ser Lys Pro Glu Glu Gly Gln Trp Ser Leu Arg Ser Gln Asp Pro Phe
 65 70 75 80
 Leu Leu Ile Phe Tyr Leu Phe Lys Pro Leu Leu Pro Pro Leu Gln Ala
 85 90 95
 Phe Pro Ser Ser Phe Thr Val Pro
 100

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TTCATCTTCT CCCTGTAAC	GAGATTTCTA CCACACCTTT	GAACAATGTT CTTTCCCTTC	60
TGGTTATCTG AAGACTGTCC	TGAAAGGAAG ACATAAGTGT	TGTGATTAGT AGAAGCTTTC	120
TAGTAGACCA TATTTCTTCT	GGATTGTAAT AAAATTGTTA	GTAGCTCCTT TTA	180
CCTGTCTCTG GAAAGCCATT	TTTGAATTGC TGATTACTTT	GGCTTTAATC AGTGGTCACC	240
TAGAAAAAGC TTTGTAATCA	TAACACAATG AGTAATTCTT	GATAAAAGTT CAGATACAAA	300
AGGAGCACTG TAAAACTGGT	AGGAGCTATG GTTTAAGAGC	ATTGGAAGTA GTTACA	360
AAGGATTTTG GTAGAAAGGT	ATGAGTTTGG TCGAAAAATT	AAAATAGTGG CAAAATAAGA	420
TTTAGTTGTG TTTTCTCAGA	GCCGCCACAA GATTGAACAA	AATGTTTTCT GTTTGGGCAT	480
CCTGAGGAAG TTGTATTAGC	TGTTAATGCT CTGTGAGTTT	AGAAAAAGTC TTGATAGTAA	540
ATCTAGTTTT TGACACAGTG	CATGAACATA GTAGTTAAAT	ATTTACATAT TCAGAAAGGA	600
ATAGTGGAAA AGGTATCTTG	GTTATGACAA AGTCATTACA	AATGTGACTA AGTCATTACA	660
AATGTGACTG AGTCATTACA	GTGGACCCTC TGGGTGCATT	GAAAAGAATC CGTTTTATAT	720
CCAGGTTTCA GAGGACCTGG	AATAATAATA AGCTTTGGAT	TTTGCATTCA GTGTAGTTGG	780
ATTTTGGGAC CTTGGCCTCA	GTGTTATTTA CTGGGATTGG	CATACGTGTT CACAGGCAGA	840
GTAGTTGATC TCACACAACG	GGTGATCTCA CAAA	ACTGGT AAGTTTCTTA	900

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CCCTCCCTTT TTTTTTTTAA TTTGGTGCCT GCAACTTTCT TAACAATGAT TCTACTTCCT      960
GGGCTATCAC ATTATAATGC TCTTGGCCTC TTTTTTGCTG CTGTTTTGCT ATTCTTAAAC      1020
TTAGGCCAAG TACCAATGTT GGCTGTTAGA AGGGATTCTG TTCATTCAAC ATGCAACTTT      1080
AGGGAATGGA AGTAAGTTCA TTTTAAAGTT GTGTTGTCAG TAGGTGCGGT GTCTAGGGTA      1140
GTGAATCCTG TAAGTTCAAA TTTATGATTA GGTGACGAGT TGACATTGAG ATTGTCCTTT      1200
TCCCTGATCA AAAAATGAAT AAAGCCTTTT TAAACAAAAA AAAAAAAAAA AAAAAAAAAA      1260
AAAAAAAAAA AAAAAA                                     1276

```

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```

Met Ile Leu Leu Pro Gly Leu Ser His Tyr Asn Ala Leu Gly Leu Phe
 1             5             10             15

Phe Ala Ala Val Leu Leu Phe Leu Asn Leu Gly Gln Val Pro Met Leu
          20             25             30

Ala Val Arg Arg Asp Ser Val His Ser Thr Cys Asn Phe Arg Glu Trp
 35             40             45

Lys

```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

GGGGCTCGTC TGTTCCAGGA GCCCTGAACC AAAGAGCAGC GGAGTTTGAG AAGCCAGCAG      60
CTCGGGGTTC GGCAGCAGCG GTCCCATCGG CTGAAGTTTCG GGGGGGGTGG GGCGCCGAGC      120
GCGCGGGGTG GGGGGGGTCC TGGTCTTTGG CTTCTCGACT CGGTCCTGTT TCGACAGCGA      180
ACATGTCGCG GCCTGTCAGA AATAGGAAGG TTGTTGATTA CTCACAGTTT CAGGAATCTG      240
ATGATGCAGA TGAAGATTAT GGAAGAGATT CGGGCCCTCC CACTAAGAAA ATTCGATCAT      300
CTCCCCGAGA AGCTAAAAAT AAGAGGCGAT CTGGAAAGAA TTCACAGGAA GATAGTGAGG      360

```

ACTCAGAAGA CAAAGATGTG AAGACCAAGA AGGATGATTC TCACTCAGCA GAGGATAGTG 420
AAGATGAAAA AGAAGATCAT AAAAATGTGC GCCAACAACG GCAGGCGGCA TCTAAAGCAG 480
CTTCTAAACA GAGAGAGATG CTCATGGAAG ATGTGGGCAG TGAGGAAGAA CAAGAAGAGG 540
AGGATGAGGC ACCATTCCAG GAGAAAGATT CCGGCAGCGA TGAAGATTTT CTAATGGAAG 600
ATGATGACGA TAGTGACTAT GGCAGTTCGA AAAAGAAAAA CAAAAAGATG GTTAAGAAGT 660
CCAAACCTGA AAGAAAAGAA AAGAAAATGC CCAAACCCAG ACTAAAGGCT ACAGTGACGC 720
CAAGTCCAGT GAAAGGCAAA GGGAAAGTGG GTCGCCCCAC AGCTTCAAAG GCATCAAAGG 780
AAAAGACTCC TTCTCCCAAA GAAGAAGATG AGGAACCGGA AAGCCCGCCA GAAAAGAAAA 840
CATCTACAAG CCCCCACCC GAGAAATCTG GGGATGAAGG GTCTGAAGAT GAAGCCCCTT 900
CTGGGGAGGA TTAAAAGTGA TGATGGTCTG GGGAGAGATT TTATTAAAAA AAAAAAGAAA 960
AAAAAAGAAA AAAGAGGGAG GAAAAAAAG AACCTACTTA AGATAGAACA TGGTTTTGGC 1020
TATGGCTTGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1080
AAAAAAAAAA AAAAAAAAAA AAAAAAAA 1108

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Met Ser Arg Pro Val Arg Asn Arg Lys Val Val Asp Tyr Ser Gln Phe
1 5 10 15
Gln Glu Ser Asp Asp Ala Asp Glu Asp Tyr Gly Arg Asp Ser Gly Pro
20 25 30
Pro Thr Lys Lys Ile Arg Ser Ser Pro Arg Glu Ala Lys Asn Lys Arg
35 40 45
Arg Ser Gly Lys Asn Ser Gln Glu Asp Ser Glu Asp Ser Glu Asp Lys
50 55 60
Asp Val Lys Thr Lys Lys Asp Asp Ser His Ser Ala Glu Asp Ser Glu
65 70 75 80
Asp Glu Lys Glu Asp His Lys Asn Val Arg Gln Gln Arg Gln Ala Ala
85 90 95
Ser Lys Ala Ala Ser Lys Gln Arg Glu Met Leu Met Glu Asp Val Gly
100 105 110
Ser Glu Glu Glu Gln Glu Glu Glu Asp Glu Ala Pro Phe Gln Glu Lys
115 120 125

Asp Ser Gly Ser Asp Glu Asp Phe Leu Met Glu Asp Asp Asp Ser
 130 135 140

Asp Tyr Gly Ser Ser Lys Lys Lys Asn Lys Lys Met Val Lys Lys Ser
 145 150 155 160

Lys Pro Glu Arg Lys Glu Lys Lys Met Pro Lys Pro Arg Leu Lys Ala
 165 170 175

Thr Val Thr Pro Ser Pro Val Lys Gly Lys Gly Lys Val Gly Arg Pro
 180 185 190

Thr Ala Ser Lys Ala Ser Lys Glu Lys Thr Pro Ser Pro Lys Glu Glu
 195 200 205

Asp Glu Glu Pro Glu Ser Pro Pro Glu Lys Lys Thr Ser Thr Ser Pro
 210 215 220

Pro Pro Glu Lys Ser Gly Asp Glu Gly Ser Glu Asp Glu Ala Pro Ser
 225 230 235 240

Gly Glu Asp

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ASTTCRAATT CGGCCTTCAT GGMCTAGCAC GGACTCTGCC TTCTAAAAGT GGAACCCCMC	60
AGTMCCAGCT GTTGCCTMAG SGTGGACASA TCAGSCGAAG CTCCTGCCCT GCCTGTTGGC	120
AGCMTCCATG GGCCAAGCTC TTGCCTCTCA CCATCCTCTC CAGGCCCAGT ACTGTTTCCA	180
GCCGGCCTCT CCAGGCCCAA CTCTCCCTCT CAGCTGTGCC TGCCGGCCCA GCTCCTACCT	240
CGCAAAGCC ACGTTCGGCC CAGCTCCTGC CCAGCTCCTG GCAGCCTTTG TAAACCCAG	300
GATCCTCTAA GTCAGGCCTT TCAGGCCCTG CCTTTGGCTC CCCGGTGGCA TGGAGAGGCC	360
CAGCTCCTGC CTGACAGCGG CCTCTCCAGG CCCAGCTCTT GCCTCACGTT GGCTCCCTG	420
GGCCACGTTT CCGCCTGCCT CGCGGCAGCC CCGACAATCC CGGCTCCTGC CTCCCGATGG	480
CATCTTTAGG CTCATCTCGT GCCTCACCAC GGCCTGCACC AGGCCACACT CCTGCCTTTC	540
GGTGGCCTCC GCGGGCCTGA CTCCTGCGTC CCAATGGCCT CTTTAGGCCC GGCTCGTGCC	600
TCGCCGCGGC CTCCTGAGGC CCACCTTTGC CTTTCTGGCA GCCTCTCCAG GCCCAGGACT	660
TCCTCAAGTC GGCCTCTGCC AGCCCAGTGG CCGCCTCCCG GCCTCCTCTC CGGGCCCAGC	720

TCCTTGCTCG TGGCTGCGCC CGCGGGCCCA GCTCCTGCCT CTGAACATCC TCCTGTGACT	780
CGGCTCCTGC CCAGCTCCCA GCGGCCTCCG TAGACCCGAA GCCTCCTCCG GTCCAGCTCT	840
CCAGGCCTGC CTCCTGCCTC GTGGCGGCCT TCCCCGGCCA TGCTCGTGCC GGCTTCCCGG	900
CAGCCTCCAC GAGCCCGGCT CCTGCCTCAC GCGGGCCCCCT CCAGGCCAG CTCGTGCCTC	960
GCGGCGGCCT CTCCAGGCC GGCTCCCGCC CAGCCCGACG GCGTCTCCCA GCCCAAGGCT	1020
CCCTTCCTCA ACGTCGGCCC CTCTGGGCCC AGCTCCTGCC TCCCGCTGAT GGCCTGTGCG	1080
GGCCACCCG AGGCGGCCCG AAGTCGGCCT CGCCAGGCC AGCTCCTGCC TGGCGTAGGC	1140
CCCTGGGGGC ACGGCCTCTG CCCMACAGTG GCCCCTCCGG GCCCAGCTCG TGCCTCGGCT	1200
TGGCCGCTC AGGCCAGCT CCTGCCTGTG GGCGGCCTCT CTCCAGACCC GGCTCTCGCC	1260
TCCCGGCATC CTCTCCAGGC CCAGAGCTGT TTCCAGTTGC TAGACCATTT TTGTGCCTGC	1320
CTCGTTGCAG CATCTCCAAG CCCAGCTTTT GCTTTTCTGC AGTTTCTTGA GGCCGAAGTC	1380
CATTTTTCGA ATGGCTTATT TAGGCCCAGC TCTTGCGTTT GCATTGTCCC TTCAGGCCCA	1440
GAAGTTTCTC ACGTCATCGT CACCAGGCCT AGCTTCTGCA TCTGGTCAGC CTTTTAAGGC	1500
CCAGCTTTTG CCTCATAAAC TCAGCTCCTG TTTAATGGCG GCCTCCCAGG TCCCACCTTC	1560
TGCCTTCCTG TGTCCACTCC AGGCCAGCT ACTGCCTTGG TGCTCTTTTT AAGTCAATAA	1620
TTTTTTCCAG TCGACCTCTC CAGGCCCAAC TTGTACCTCT GAGTGTCTC TAGGATCTCA	1680
GCTTCTGCCT AACAAATGACC TCTTTAGACT CAGCTCATTT TCACTGCTAC ATCTTCAAGC	1740
CATTCTCCTG CCTCTTGGA ACCTCTAGTG GCCCAGCTTC TGCCTCACAG CAGCCTCTCC	1800
ATGCATGCCT AGCTCCTGCC TCTTTAGGGA ACTTACAGGC CTAAAGCTTT CTTAATTTGG	1860
GCTTCTCAAG CCCAGCTCCT GCCTTCTGTT GGGCTCTACA GGCCTGGCAT CATCCTTTCA	1920
ACAGCCTCTT TAGGCCCGGC CTCTCCAGGA CAAAACATC CTTAAGTCAA CCTCACCAGG	1980
CCCGGCTCCT GTCTCCTTGC GGCTCCAGA GGCCGAGCTT TTGCCTGCCA ATGGCCTCTC	2040
TAGCCCCAGC TTTTGCCTGC CAATGGCCTC TCTAGCCCCA GCTTCTGCCT TTCATCGGTC	2100
TCTCCAGGCT TAGCTCCTTT CTCTTCACGG CCTCTGCAGG CCTAAAGCTT CCTCAATTTG	2160
GCATCTCCAG GCCCAGCTCC TGCTCCAGG CCGCCTCTGC AGGCCTATCT CAAGCCTTAC	2220
AACAGCCTCT TTACCCCCAG CTCCTTTCTC CGACTTGTCT CTCCAGGCCT AGAAGCTCCT	2280
CATGTTTACC TCACCAGGCC CACCTCCTGC CTTCCAGTAG CGTCTACAAG TTTGGCTCCT	2340
GCCTCCCATG GATCTCTCCA GGCCCCAAAC TTTCTCAAGT CAACCTCACC AGGCCCGGCT	2400
TCTCCCTTTC ATCAGCCTTC CAAAGGCCAG CTTTGTGCTT ATGTCTGCCT TCCGAGTCCC	2460
AGCTCCTGTT TTATGGCAGC CTCCTGAGGC CCAGCTCCTG CCTCCTAGTG GCCTCTTTTG	2520
GCCCAACTCT TTCCTACCA GGGCCTTCCA GACCAGTTC CTGCCTTTTA GCAGCCACTA	2580

CAGGCCCAGC TTTGCGTCCT TTCAAGAGTC CTGCCTCACA GTGGCCTCCC AAGGGCAACT 2640
 TTCTGCCTCA TGTCAGCCTC TTGTGCCCTG GTCCTGCTTC CTGGTAGACT CTGCAGGCCC 2700
 TGCTCCTGCC TTACGTTGCC CCTTTTATAA AGATCCAGTT CCTGCCTCCT GGCTGCCTCT 2760
 ATGAGCCCCAA ATCCTGCCTA ACAACAACCT GTTTTTGCCC AGCTCCTGCT TCCTGGCAGC 2820
 CTCCTTAGGC CAAAAATTTT CTTCAATTGA CCTCTCCAGG CCCAGCTCCT GCCTCTCAGC 2880
 ACCCTCTTTA GGCCCAGCTC CTGCCTTAAT AAATTTGAAT AAATTATTGT TATGTGAAAA 2940
 AAAAAAAAAA AA 2952

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Met Ala Tyr Leu Gly Pro Ala Leu Ala Phe Ala Leu Ser Leu Gln Ala
 1 5 10 15
 Gln Asn Phe Leu Thr Ser Ser Ser Pro Gly Leu Ala Ser Ala Ser Gly
 20 25 30
 Gln Pro Phe Lys Ala Gln Leu Leu Pro His Lys Leu Ser Ser Cys Leu
 35 40 45
 Met Ala Ala Ser Gln Val Pro Pro Ser Ala Phe Leu Cys Pro Leu Gln
 50 55 60
 Ala Gln Leu Leu Pro Trp Cys Ser Phe
 65 70

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1294 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GTGCCCCGCC GCTGCTGTCA CCCCCGGCCG CTGCTGCCCT CCCC GCCGAG GTTCTACTGC 60
 TCTCCTTCTT AAGAAGGGTG GGAGGCACTC GGTCTCTCCC CACACCTCTC GCCTGAGGCC 120
 AGGCGCCAGG TGTCGCCTGA AGCCAGACAG CCGGTTTGGG AGCGAGCCTG AGGTCAACCA 180
 ATCAATGGCT CAGACAGATA AGCCAACATG CATCCCGCCG GAGCTGCCGA AAATGCTGAA 240

GGAGTTTGCC AAAGCCGCCA TTCGGGCGCA GCCGCAGGAC CTCATCCAGT GGGGGGCCGA 300
 TTATTTTGAG GCCCTGTCCC GTGGAGAGAC GCCTCCGGTG AGAGAGCGGT CTGAGCGAGT 360
 CGCTTTGTGT AACTGGGCAG AGCTAACACC TGAGCTGTTA AAGATCCTGC ATTCTCAGGT 420
 TGCTGGCAGA CTGATCATCC GTGCAGAGGA GCTGGCCCAG ATGTGGAAAG TGGTGAATCT 480
 CCCAACAGAT CTGTTTAATA GTGTGATGAA TGTGGGTCGC TTCACGGAGG AGATCGAGTG 540
 GCTGAAGTTT TTAGCCCTTG CTTGCAGCGC TCTGGGAGTT GTAAGTTAGC TTGACTGTTT 600
 TTTGTTCTTG AAGGGGAAAT CTCCCTCTGG GCCTGGAAGG GCAGTGCATC TATACACGCG 660
 GTCAACTCTG CAGGGCTGAT GATAAACATG CCTCTTCTCC TATTGTCCTT CTCCTCTCTA 720
 AAGCAAGGTC ATTTCTGTGC TCGTCAGGCA GTGGCAGGGG TTGGGAGGAG GAGAGAGGGA 780
 AACACTGTGG TCAGGCTCTG GGGAGAGTTG ACTACAGTGT AGCTCTTGGA TTATTTATGA 840
 ATATTGCCCT CAGATTTATT TTCACTCTGC TCCTTCCATT CATATTCCCA GAGACAACCA 900
 AGAGCCGACT GTAGAAAAAG ACTTCCAGAC ACCTAGAATA TATATCAATA GACACTGTTT 960
 AAAAGGGGTA CAATCTTATA GAAAACTATG TAATAAACAG AATTGGATGC AGAACTCAGA 1020
 CATAAGAAAG CAAAAACAAA GAGAGATGAG GCTATTTCTG AATTTAGTCA TGACATCTCC 1080
 ATGGATACAG GATGTTTATA CAGATTTATG CCTTTTCCAA ATTTGACTTG TTTGATATTG 1140
 GAAAAACAAT TTTACTGTTT TGAAGCCAAA GATGTTGAAA TCAGTTTATA TGTATAGATA 1200
 TTTAAAGCTT GGGTATCTTA TATGTGGACT TACATTGTTA AACATTGTTA AAATAAAATG 1260
 AATCAAAAAC ATGGTTTTTTA AAAAAAAAAA AAAA 1294

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Ala Gln Thr Asp Lys Pro Thr Cys Ile Pro Pro Glu Leu Pro Lys
 1 5 10 15
 Met Leu Lys Glu Phe Ala Lys Ala Ala Ile Arg Ala Gln Pro Gln Asp
 20 25 30
 Leu Ile Gln Trp Gly Ala Asp Tyr Phe Glu Ala Leu Ser Arg Gly Glu
 35 40 45
 Thr Pro Pro Val Arg Glu Arg Ser Glu Arg Val Ala Leu Cys Asn Trp
 50 55 60

Ala Glu Leu Thr Pro Glu Leu Leu Lys Ile Leu His Ser Gln Val Ala
65 70 75 80

Gly Arg Leu Ile Ile Arg Ala Glu Glu Leu Ala Gln Met Trp Lys Val
85 90 95

Val Asn Leu Pro Thr Asp Leu Phe Asn Ser Val Met Asn Val Gly Arg
100 105 110

Phe Thr Glu Glu Ile Glu Trp Leu Lys Phe Leu Ala Leu Ala Cys Ser
115 120 125

Ala Leu Gly Val Val Ser
130

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

TTTTTTTTTT TTTTGTATA GCAATGGAAG AATGGCCTCG TACACACGCT AGAGTGGAAA	60
GTCCCAGGCA CCAAGGCTTC CCACCCTAGA AGCAAGCTCA GGGCTTTCTC TTCATCCTTC	120
CAGGGAGAGC ACTGAGAGAT GATGGGGGGT TGGCAGGGGG CATCCCTTGG ATTATCATTC	180
TCCAGACTTA GGCTTGGAGG GGAGGGTGGA GAAGTGGATT TCTGGGTCTG GTCCACCTCA	240
CCTGTTTTCT CAGCTTCTCA CCCACTCAGA GCTCTTGCCC CAATTCTCCC TTTCATCCTG	300
CAGATCCCTG CGCCTGACTC ATCTCAGGCG AGGAGGCAAA TCATCAGTTA TCTCAGGCAG	360
CAGCAGGACG AGACTCCTTT CTGATTTTCT CCTTCCCTGG CCACCTCTCC CCACCCCAT	420
TTCACTCATT CCAAACCTCT GGCTCCCCA GCAACTCTAC ATCCTCATCT CCACCTGTTC	480
CCTCTCTCGA TGCTGTGGGT GACGTTGGAG AGGGAAGCCC GGAGCCCTGA CCTAGTCCGG	540
CGTGGAGAGA GGAATGGAAA GCAGTGTCCT TTTTGAGAAG GCAAATTTAC AGCTGGCTTT	600
TGTAATCCTA GCTATTTTTT GTTTGTTTGC TAAGTCTTTG ATAGTCCCCA GTGTGGTTTG	660
TCTGCCAGTG ATCTCAGCAC CACCAGAGAG CTTGTTAGAA ATGCGGCATC CCAACCCAC	720
CACAGCCCTC CCAAGTCAGA TACTGCCACC TCACGAGGCC CCCAGGGAT CCACAAGTTC	780
ATTAAAGTTT CAGGAATCCA ATTCTACTAC AAAATATACA TTTATAATTA GGAAAAGGAT	840
AGTTCTTTTA AATGGTAGAA CTTCCCCAAT GAGTCAGCTA CCTGTATTTT TGGCCTGTCA	900
GGCTAGACAC TGGAGACCAT TCTGCATAGA ATTGTACCTC CCTGAACTAC TGTTAGGCCT	960
TAGGGTGGGG ATTCATCTTT CCCTTCTCCC CACCATGGAG ACAAATCCT CTTAAACATA	1020
TCCGGGCCTG GCATGGTGGY TMACGCCTCG GCCTCCCAA GTTCTGGGAT TACAGGCATG	1080

AGCCAYTGTG CCCAGCCACC CGTCACCTGY TAGTGTAGAC AAATGAATAA ACTTAGACAA 1140
 GCACATGGGC TCCCTCTATA CCAGCCTAGA CTTTGACACT GAAACTCCAT GAGTCTGGGC 1200
 CACTTCCTGC CACAAGTGTG AATGGAAAAT AAATCATTTT CCAAGGAACC CAAAATCACT 1260
 AAGCCAAGGA GTCAAGCTGA GAACTTTCAG GCAAACCTGC CCCCCATTTT ATTCCTTAA 1320
 TAAGAGAGCT ACAAAGATTA AAAAAAAAAA AAAA 1354

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Met Glu Ser Ser Val Pro Phe Glu Lys Ala Asn Leu Gln Leu Ala Phe
 1 5 10 15
 Val Ile Leu Ala Ile Phe Cys Leu Phe Ala Lys Ser Leu Ile Val Pro
 20 25 30
 Ser Val Val Cys Leu Pro Val Ile Ser Ala Pro Pro Glu Ser Leu Leu
 35 40 45
 Glu Met Arg His Pro Asn Pro Thr Thr Ala Leu Pro Ser Gln Ile Leu
 50 55 60
 Pro Pro His Glu Ala Pro Gln Gly Ser Thr Ser Ser Leu Lys Phe Gln
 65 70 75 80
 Glu Ser Asn Ser Thr Lys Tyr Thr Phe Ile Ile Arg Lys Arg Ile
 85 90 95
 Val Leu Leu Asn Gly Arg Thr Ser Pro Met Ser Gln Leu Pro Val Phe
 100 105 110
 Leu Ala Cys Gln Ala Arg His Trp Arg Pro Phe Cys Ile Glu Leu Tyr
 115 120 125
 Leu Pro Glu Leu Leu Leu Gly Leu Arg Val Gly Ile His Leu Ser Leu
 130 135 140
 Leu Pro Thr Met Glu Thr Lys Ser Ser
 145 150

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CCCCGGTCCC CGCCGCAGCC GCTGCATCCT CCGTGCCCGG CCTGAGCTGG AGTCCCCCGC	60
GCCCCCGCG TTCCGCCCGG CCATGGCTGC GGTGGCGCTG ATGCCACCGC CGCTGCTGCT	120
GCTGCTGCTG TTGGCGTCGC CGCCCGCCGC CTCCGCGCCG TCCGCCCGCG ATCCCTTCGC	180
CCCCCAGCTC GGGGACACGC AGAACTGCCA GCTGCGGTGC CGCGACCGCG ACCTCGGCCC	240
GCAGCCCTCG CAGGCGGGGC TGGAGGGCGC CTCCGAGTCT CCCTATGACA GAGCCGTTCT	300
GATCAGCGCT TGCGAGCGTG GCTGCCGCCT CTTCTCCATC TGCCGATTTG TGGCCAGAAG	360
CTCCAAGCCC AATGCCACCC AAAGTGAAGT TGAAGCAGCC TGCGTGGAAG CCTATGTGAA	420
GGAGGCAGAR CAGCAGGCCT GTAGCCACGG CTGCTGGAGC CAGCCCGCGG AGCCTGAGCC	480
GGARCAGAAG AGAAAGGTCC TGGAGGCTCC AAGTGGGGCC CTCTCCCTCT TGGACTTGTT	540
TTCCACCCTC TGCAATGACC TTGTCAACTC AGCCCAGGGA TTTGTCTCCT CCACCTGGAC	600
ATACTACTTG CAGACTGACA ATGGGAAAGT GGTGGTGTTC CAGACTCAGC CCATAGTGGA	660
GAGCCTCGGC TTCCAGGGGG GCCGTCTGCA GCGCGTGGAG GTGACCTGGC GAGGCTCCCA	720
CCCTGAAGCC CTGGAGGTGC ACGTGGACCC TGTAGGCCCC CTGGACAAGG TGAGGAAGGC	780
CAAGATCCGA GTCAAGACCA GCAGCAAGGC CAAGGTGGAG TCTGAAGAGC CACAGGACAA	840
TGACTTCCTC AGTTGCATGT CCCGGCGCTC GGGTCTGCCT CGCTGGATCC TGGCCTGCTG	900
CCTCTTCCTC TCCGTGCTGG TGATGCTGTG GCTGAGCTGC TCCACCCTGG TGACCGCGCC	960
TGGCCAGCAC CTCAAGTTCC AGCCTCTGAC CCTGGAGCAG CACAAGGGCT TCATGATGGA	1020
GCCCGATTGG CCCCTGTACC CGCCGCCGTC CCACGCCTGT GAGGACAGCC TACCACCCTA	1080
CAAGCTGAAG CTGGACCTGA CCAAGCTGTA GGCCTCCACT GGCCCCATCA CTGCCAACTG	1140
CAGGGGGCCC CTCGGGCCTC ACTTGCCCTG AGCCCAGGAG TCCAAGGGCA GGGTGGGTCC	1200
AGCGTTGAGC CCCTCCACCC CCAAATCCTT CCTCTCCTCC CAGTCCCACC CCTTGCCCCA	1260
CGGAGTCCTG GGGACGCAGT GCCCCAGCTG GGAAGAGGGC GGGATCGGGC ACTGGTTCCT	1320
CCTTGTCCTC GCTTTCTTGG GGGCTTGCTA CTTTTTGTCT TCTATTGTGT GGCTTTCTGA	1380
GTATTTGAAC CCCAGTCCTG TGTCACCTTC CTTTTTCCTT CTATGTCCCC TCTCTGCGGG	1440
GGGGGCGCTG AGGCTGAGGG GGAGCTGCGT CTTGCTAGGG CTTCCCCCTT CTCCCCATCC	1500
CGGTCTCCAG AGACCCAGCT TCTGAGAGAC AGGGTGTGGG CATCTCCATG CCCCTATAAA	1560
GCGTGCCTGG GGCTTGCTCTG GGGCTGGGGA GGAATAAACC ATGTATATAA AAGAAAAAAA	1620
AAAAAAA	1628

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met	Ala	Ala	Val	Ala	Leu	Met	Pro	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Ala	Ser	Pro	Pro	Ala	Ala	Ser	Ala	Pro	Ser	Ala	Arg	Asp	Pro	Phe	20	25	30	
Ala	Pro	Gln	Leu	Gly	Asp	Thr	Gln	Asn	Cys	Gln	Leu	Arg	Cys	Arg	Asp	35	40	45	
Arg	Asp	Leu	Gly	Pro	Gln	Pro	Ser	Gln	Ala	Gly	Leu	Glu	Gly	Ala	Ser	50	55	60	
Glu	Ser	Pro	Tyr	Asp	Arg	Ala	Val	Leu	Ile	Ser	Ala	Cys	Glu	Arg	Gly	65	70	75	
Cys	Arg	Leu	Phe	Ser	Ile	Cys	Arg	Phe	Val	Ala	Arg	Ser	Ser	Lys	Pro	85	90	95	
Asn	Ala	Thr	Gln	Thr	Glu	Cys	Glu	Ala	Ala	Cys	Val	Glu	Ala	Tyr	Val	100	105	110	
Lys	Glu	Ala	Glu	Gln	Gln	Ala	Cys	Ser	His	Gly	Cys	Trp	Ser	Gln	Pro	115	120	125	
Ala	Glu	Pro	Glu	Pro	Glu	Gln	Lys	Arg	Lys	Val	Leu	Glu	Ala	Pro	Ser	130	135	140	
Gly	Ala	Leu	Ser	Leu	Leu	Asp	Leu	Phe	Ser	Thr	Leu	Cys	Asn	Asp	Leu	145	150	155	
Val	Asn	Ser	Ala	Gln	Gly	Phe	Val	Ser	Ser	Thr	Trp	Thr	Tyr	Tyr	Leu	165	170	175	
Gln	Thr	Asp	Asn	Gly	Lys	Val	Val	Val	Phe	Gln	Thr	Gln	Pro	Ile	Val	180	185	190	
Glu	Ser	Leu	Gly	Phe	Gln	Gly	Gly	Arg	Leu	Gln	Arg	Val	Glu	Val	Thr	195	200	205	
Trp	Arg	Gly	Ser	His	Pro	Glu	Ala	Leu	Glu	Val	His	Val	Asp	Pro	Val	210	215	220	
Gly	Pro	Leu	Asp	Lys	Val	Arg	Lys	Ala	Lys	Ile	Arg	Val	Lys	Thr	Ser	225	230	235	
Ser	Lys	Ala	Lys	Val	Glu	Ser	Glu	Glu	Pro	Gln	Asp	Asn	Asp	Phe	Leu	245	250	255	
Ser	Cys	Met	Ser	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Trp	Ile	Leu	Ala	Cys	260	265	270	

Cys Leu Phe Leu Ser Val Leu Val Met Leu Trp Leu Ser Cys Ser Thr
 275 280 285

Leu Val Thr Ala Pro Gly Gln His Leu Lys Phe Gln Pro Leu Thr Leu
 290 295 300

Glu Gln His Lys Gly Phe Met Met Glu Pro Asp Trp Pro Leu Tyr Pro
 305 310 315 320

Pro Pro Ser His Ala Cys Glu Asp Ser Leu Pro Pro Tyr Lys Leu Lys
 325 330 335

Leu Asp Leu Thr Lys Leu
 340

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TCGGGCGGCG GAGTAGCAAG TGGCCATGGG GAGCCTCAGC GGTCTGCGCC TGGCAGCAGG	60
AAGCTGTTTT AGGTTATGTG AAAGAGATGT TTCCTCATCT CTAAGGCTTA CCAGAAGCTC	120
TGATTTGAAG AGAATAAATG GATTTTGCAC AAAACCACAG GAAAGTCCCG GAGCTCCATC	180
CCGCACTTAC AACAGAGTGC CTTTACACAA ACCTACGGAT TGGCAGAAAA AGATCCTCAT	240
ATGGTCAGGT CGCTTCAAAA AGGAAGATGA AATCCCAGAG ACTGTCTCGT TGGAGATGCT	300
TGATGCTGCA AAGAACAAGA TGCGAGTGAA GATCAGCTAT CTAATGATTG CCCTGACGGT	360
GGTAGGATGC ATCTTCATGG TTATTGAGGG CAAGAAGGCT GCCCAAAGAC ACGAGACTTT	420
AACAAGCTTG AACTTAGAAA AGAAAGCTCG TCTGAAAGAG GAAGCAGCTA TGAAGGCCAA	480
AACAGAGTAG CAGAGGTATC CGTGTTGGCT GGATTTTGAA AATCCAGGAA TTATGTTATA	540
ACGTGCCTGT ATTAAAAAGG ATGTGGTATG AGGATCCATT TCATAAAGTA TGATTTGCCC	600
AAACCTGTAC CATTTCCGTA TTTCTGCTGT AGAAGTAGAA ATAAATTTTC TTAAATAAAA	660
AAAAAAAAA A	671

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Met	Gly	Ser	Leu	Ser	Gly	Leu	Arg	Leu	Ala	Ala	Gly	Ser	Cys	Phe	Arg	
1				5					10					15		
Leu	Cys	Glu	Arg	Asp	Val	Ser	Ser	Ser	Leu	Arg	Leu	Thr	Arg	Ser	Ser	
			20					25					30			
Asp	Leu	Lys	Arg	Ile	Asn	Gly	Phe	Cys	Thr	Lys	Pro	Gln	Glu	Ser	Pro	
		35					40					45				
Gly	Ala	Pro	Ser	Arg	Thr	Tyr	Asn	Arg	Val	Pro	Leu	His	Lys	Pro	Thr	
	50					55					60					
Asp	Trp	Gln	Lys	Lys	Ile	Leu	Ile	Trp	Ser	Gly	Arg	Phe	Lys	Lys	Glu	
65					70					75					80	
Asp	Glu	Ile	Pro	Glu	Thr	Val	Ser	Leu	Glu	Met	Leu	Asp	Ala	Ala	Lys	
				85					90					95		
Asn	Lys	Met	Arg	Val	Lys	Ile	Ser	Tyr	Leu	Met	Ile	Ala	Leu	Thr	Val	
			100					105					110			
Val	Gly	Cys	Ile	Phe	Met	Val	Ile	Glu	Gly	Lys	Lys	Ala	Ala	Gln	Arg	
		115					120					125				
His	Glu	Thr	Leu	Thr	Ser	Leu	Asn	Leu	Glu	Lys	Lys	Ala	Arg	Leu	Lys	
	130					135						140				
Glu	Glu	Ala	Ala	Met	Lys	Ala	Lys	Thr	Glu							
145					150											

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CACAAGAGGA GTTACTTGTT CCAGCCTCCT GTGTGGACTG CTTTCCTATC AAAGCACCTT	60
AGACATGCAC GAGGAAGAAA TATACACCTC TCTTCAGTGG GATAGCCCAG CACCAGACAC	120
TTACCAGAAA TGTCTGTCTT CCAACAAATG TTCAGGAGCA TGCTGTCTTG TGATGGTGAT	180
TTCATGTGTT TTCTGCATGG GATTATTAAC GGCATCCATT TTCTTGGGCG TCAAGTTGTT	240
GCAGGTGTCC ACCATTGCGA TGCAGCAGCA AGAAAACTC ATCCAACAAG AGAGGGCACT	300
GCTAAACTTT ACAGAATGGA AGAGAAGCTG TGCCCTTCAG ATGAAATATT GCCAAGCCTT	360
CATGCAAAAC TCATTAAGTT CAGGATTTTA TCACTGGCAG CTTGAGGAAG ATTAAGGAA	420
GCTATGATTA CTGGGTGGGG TTGTCTCAGG ATGGACACAG CGGACGCTGG CTTTGGCAAG	480
ATGGCTCCTC TCCTTCTCCT GGCCTGTTGC CAGCAGAGAG ATCCCAGTCA GCTAACCAAG	540

TCTGTGGATA CGTGAAAAGC AATTCCCTTC TTTCGTCTAA CTGCAGCACG TGGAAGTATT 600
 TTATCTGTGA GAAGTATGCG TTGAGATCCT CTGTCTGAAA GAAATTGTGT TCAAAGTGTT 660
 CTATTACACT GTTATTTTGA GCATGCCATT GGAAAACCCA CCCCACCCC CCCTCAAAAA 720
 AACAGAACAG TAAACCAAAA TGTGGGCCAT GAAATTAGCA ACCTGGGACT CAATAATACA 780
 CTTGGGAATA TTCTTCACA CCGTCCAGAT TTCATTTGAT GTTGTTTACA TTGCAAGAGT 840
 AAAACTTATT TAGAGCTACA GAAGACAAAA CCCTGAAGAG TTAAGAACAA ACGCAAGGAA 900
 ATAATTTTTA TTGTTTAAAG CCCGGAATGA CTGTAACCTT CACACAAGGT ACGCATCTAT 960
 GTTTTTGGGG GAGGTGATGT AGTTACAGCT GACTAATATT TTTAAAATAA ATAAATAAAT 1020
 TTGGCCTTTA AAACCTCAAAA AAAAAAAAAA AAAAAA 1056

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Met His Glu Glu Glu Ile Tyr Thr Ser Leu Gln Trp Asp Ser Pro Ala
 1 5 10 15
 Pro Asp Thr Tyr Gln Lys Cys Leu Ser Ser Asn Lys Cys Ser Gly Ala
 20 25 30
 Cys Cys Leu Val Met Val Ile Ser Cys Val Phe Cys Met Gly Leu Leu
 35 40 45
 Thr Ala Ser Ile Phe Leu Gly Val Lys Leu Leu Gln Val Ser Thr Ile
 50 55 60
 Ala Met Gln Gln Gln Glu Lys Leu Ile Gln Gln Glu Arg Ala Leu Leu
 65 70 75 80
 Asn Phe Thr Glu Trp Lys Arg Ser Cys Ala Leu Gln Met Lys Tyr Cys
 85 90 95
 Gln Ala Phe Met Gln Asn Ser Leu Ser Ser Gly Phe Tyr His Trp Gln
 100 105 110
 Leu Glu Glu Asp
 115

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

ANATTAGATC TGTTTCCATT TCCCAGGCA

29

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TNGCGTGAGA TCAACTACTC TGCCTGTGA

29

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

ANACAGGACC GAGTCGAGAA GCCAAAGAC

29

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

ANGGGACAAT GCAAACGCAA GAGCTGGGC

29

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ANGAGGCATG TTTATCATCA GCCCTGCAG

29

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

ANATTTGCCT TCTCAAAGG GACACTGCT

29

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GNTGGGACTG GGAGGAGAGG AAGGATTTG

29

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GNAACGCCAT AAGCATGTCC TTCTAATGT

29

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

ATTY DOCKET NO.: GIN-6054CP

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CNTGAAATCA CCATCACAAG ACAGCATGC

29

ATTYDOCKETNO:GIN-6054CP

1

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